

In the Specification

On page 1, line 26, please insert new paragraph as follows:

--SUBMISSION ON COMPACT DISC

The contents of the following submission on compact discs are incorporated herein by reference in its entirety: A compact disc copy of the Sequence Listing (COPY 1) (file name: 2002420, date recorded: February 16, 2002, size: 569 KB); a duplicate compact disc copy of Sequence Listing (COPY 2) (file name: 2002420, date recorded: February 16, 2002, size: 569 KB); a computer readable form copy of the Sequence Listing (CRF COPY) (file name: 2002420, date recorded: February 16, 2002, size: 569 KB).--

In the Sequence Listing

Please insert the attached compact disc copy of the Sequence Listing on CD-R (COPY 1) in the above-captioned application. A duplicate compact disc copy of the Sequence Listing on CD-R (COPY 2) and a computer readable form copy of the Sequence Listing on CD-R (CRF COPY) accompany this response.

AMENDMENTS

In the Specification:

Please replace the paragraph beginning at page 7, line 21, with the following rewritten paragraph:

-- **Figure 1. 101P3A11 SSH sequence (SEQ ID NO:2960).** The 101P3A11 SSH sequence.--

Please replace the paragraph beginning at page 7, line 22, with the following rewritten paragraph:

-- **Figures 2A-2D. The cDNA (SEQ ID. NO. :2961) and amino acid sequence (SEQ ID. NO. :2962) of 101P3A11.** The start methionine is underlined. The open reading frame extends from nucleic acid 133 to 1086 including the stop codon (the codon for the initial M is omitted as the shorter peptide has a more favorable Kozak sequence).--

Please replace the paragraph beginning at page 7, line 26, with the following rewritten paragraph:

--**Figure 3. Amino acid sequence of 101P3A11 (SEQ ID. NO. :piece of 2962).** The 101P3A11 protein has 317 amino acids.--

Please replace the paragraph beginning at page 7, line 28, with the following rewritten paragraph:

--**Figure 4. Alignment of 101P3A11 (Sbjct) (SEQ ID NO: 2964) with mouse olfactory receptor S25 (Query.) (SEQ ID NO: 2963)** The transmembrane regions of 101P3A11 and mouse olfactory receptor S25 (ORS25) predicted using the TMHMM algorithm are highlighted in gray. The amino acids of ORS25 predicted (Floriano, W.B., et al, 2000, Proc. Natl. Acad. Sci., USA, 97:10712-10716) to be involved in binding of the ligand hexanol and/or involved in the formation of the ligand binding pocket are italicized and bolded in the Figure, and are: Leu 131, Val 134, Val 135, Gly 138, Thr139, Ser 193, Ser 197, Phe 225, Ala 230, Ile 231, Gly 234, Thr 284, Phe 287, Gln 300, Lys 302.--

Please replace the paragraph beginning at page 11, line 31, with the following rewritten paragraph:

--**Figure 23.** Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2965) with the rat (SEQ ID NO: 2966) GPCR RA1C (gi|3420759). Identities = 179/299 (59%), Positives = 231/299 (76%), Gaps = 1/299 (0%).--

Please replace the paragraph beginning at page 12, line 1, with the following rewritten paragraph:

--**Figure 24.** Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2967) with the human prostate specific GPCR (SEQ ID NO: 2968) (gi|13540539). Identities = 179/299 (59%), Positives = 233/299 (77%), Gaps = 1/299 (0%).--

Please replace the paragraph beginning at page 12, line 3, with the following rewritten paragraph:

--**Figure 25.** Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2969) with human olfactory receptor 5II12, HOR5 (SEQ ID NO: 2970) (gi|14423836). Identities = 163/304 (53%), Positives = 214/304 (69%), Gaps = 1/304 (0%).--

Please replace the paragraph beginning at page 36, line 20, with the following rewritten paragraph:

--Also, different MHC class I molecules prefer a different length of ligands. For example, SYFPEITHI offers predictions for H2-Kb octamers, HLA-A*0201 nonamers and decamers, or HLA-B8 octamers and nonamers. The maximal scores vary between different MHC alleles. Therefore, one can include known ligands/epitopes in order to have an approximation of the scoring. For example, the maximal score for HLA-A*0201 peptides is 36. The well-known epitope GILGFVFTL (SEQ ID NO: 1401) derived from the influenza A matrix protein scores 30. All predicted MHC class II ligands are 15mers, consisting of three N-terminal flanking residues, the nonamer core sequence located within the binding groove, and three C-terminal flanking residues. Thus, anchor residue P1 appears in position 4 of the peptides predicted with "SYFPEITHI".--

Please replace the paragraph beginning at page 37, line 25, with the following rewritten paragraph:

--In an embodiment described in the examples that follow, 101P3A11 can be conveniently expressed in cells (such as 293T cells) transfected with a commercially available expression vector such as a CMV-driven expression vector encoding 101P3A11 with a C-terminal 6XHis (SEQ ID NO: 1402) and MYC tag (pcDNA3.1/mycHIS, Invitrogen or Tag5, GenHunter Corporation, Nashville TN). The Tag5 vector provides an IgGK secretion signal that can be used to facilitate the production of a secreted 101P3A11 protein in transfected cells. The secreted HIS-tagged 101P3A11 in the culture media can be purified, e.g., using a nickel column using standard techniques.--

Please replace the paragraph beginning at page 70, line 3, with the following rewritten paragraph:

--In certain embodiments, the T helper peptide is one that is recognized by T helper cells present in a majority of a genetically diverse population. This can be accomplished by selecting peptides that bind to many, most, or all of the HLA class II molecules. Examples of such amino acid bind many HLA Class II molecules include sequences from antigens such as tetanus toxoid at positions 830-843 (QYIKANSKFIGITE; (SEQ ID NO: 1403), *Plasmodium falciparum* circumsporozoite (CS) protein at positions 378-398 (DIEKKIAKMEKASSVFNVVNS; (SEQ ID NO: 1404), and *Streptococcus* 18kD protein at positions 116-131 (GAVDSILGGVATYGAA; (SEQ ID NO: 1405). Other examples include peptides bearing a DR 1-4-7 supermotif, or either of the DR3 motifs.--

Please replace the paragraph beginning at page 70, line 11, with the following rewritten paragraph:

--Alternatively, it is possible to prepare synthetic peptides capable of stimulating T helper lymphocytes, in a loosely HLA-restricted fashion, using amino acid sequences not found in nature (*see, e.g.*, PCT publication WO 95/07707). These synthetic compounds called Pan-DR-binding epitopes (*e.g.*, PADRE™, Epimmune, Inc., San Diego, CA) are designed to most preferably bind most HLA-DR (human HLA class II) molecules. For instance, a pan-DR-

binding epitope peptide having the formula: aKXVAAWTLKAAa (SEQ ID NO: 1406), where "X" is either cyclohexylalanine, phenylalanine, or tyrosine, and a is either D-alanine or L-alanine, has been found to bind to most HLA-DR alleles, and to stimulate the response of T helper lymphocytes from most individuals, regardless of their HLA type. An alternative of a pan-DR binding epitope comprises all "L" natural amino acids and can be provided in the form of nucleic acids that encode the epitope.--

Please replace the paragraph beginning at page 80, line 16, with the following rewritten paragraph:

--Single chain antibodies comprise the variable domains of the heavy and light chain joined by a flexible linker polypeptide, and are expressed as a single polypeptide. Optionally, single chain antibodies are expressed as a single chain variable region fragment joined to the light chain constant region. Well-known intracellular trafficking signals are engineered into recombinant polynucleotide vectors encoding such single chain antibodies in order to precisely target the intrabody to the desired intracellular compartment. For example, intrabodies targeted to the endoplasmic reticulum (ER) are engineered to incorporate a leader peptide and, optionally, a C-terminal ER retention signal, such as the KDEL (SEQ ID NO: 1407) amino acid motif. Intrabodies intended to exert activity in the nucleus are engineered to include a nuclear localization signal. Lipid moieties are joined to intrabodies in order to tether the intrabody to the cytosolic side of the plasma membrane. Intrabodies can also be targeted to exert function in the cytosol. For example, cytosolic intrabodies are used to sequester factors within the cytosol, thereby preventing them from being transported to their natural cellular destination.--

Please replace the paragraph beginning at page 86, line 29, with the following rewritten paragraph:

--pGEX Constructs: To generate recombinant 101P3A11 proteins in bacteria that are fused to the Glutathione S-transferase (GST) protein, all or parts of the 101P3A11 cDNA protein coding sequence are fused to the GST gene by cloning into pGEX-6P-1 or any other GST- fusion vector of the pGEX family (Amersham Pharmacia Biotech, Piscataway, NJ). These constructs allow controlled expression of recombinant 101P3A11 protein sequences with GST fused at the amino-terminus and a six histidine epitope (6X His) (SEQ ID NO: 1402) at the carboxyl-

terminus. The GST and 6X His tags permit purification of the recombinant fusion protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-GST and anti-His antibodies. The 6X His tag (SEQ ID NO: 1402) is generated by adding 6 histidine (SEQ ID NO: 1402) codons to the cloning primer at the 3' end, e.g., of the open reading frame (ORF). A proteolytic cleavage site, such as the PreScissionTM recognition site in pGEX-6P-1, can be employed that permits cleavage of the GST tag from 101P3A11-related protein. The ampicillin resistance gene and pBR322 origin permit selection and maintenance of the pGEX plasmids in *E. coli*. In one embodiment, amino acids 86-317 are cloned into the pGEX-2T expression vector, the protein is expressed and purified.--

Please replace the paragraph beginning at page 87, line 8, with the following rewritten paragraph:

--pMAL Constructs: To generate, in bacteria, recombinant 101P3A11 proteins that are fused to maltose-binding protein (MBP), all or parts of the 101P3A11 cDNA protein coding sequence are fused to the MBP gene by cloning into the pMAL-c2X and pMAL-p2X vectors (New England Biolabs, Beverly, MA). These constructs allow controlled expression of recombinant 101P3A11 protein sequences with MBP fused at the amino-terminus and a 6X His (SEQ ID NO: 1402) epitope tag at the carboxyl-terminus. The MBP and 6X His tags (SEQ ID NO: 1402) permit purification of the recombinant protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-MBP and anti-His antibodies. The 6X His (SEQ ID NO: 1402) epitope tag is generated by adding 6 histidine (SEQ ID NO: 1402) codons to the 3' cloning primer. A Factor Xa recognition site permits cleavage of the pMAL tag from 101P3A11. The pMAL-c2X and pMAL-p2X vectors are optimized to express the recombinant protein in the cytoplasm or periplasm respectively. Periplasm expression enhances folding of proteins with disulfide bonds. In one embodiment, amino acids 86-310 is cloned into the pMAL-c2X expression vector, the protein is expressed and purified.--

Please replace the paragraph beginning at page 87, line 20, with the following rewritten paragraph:

--pET Constructs: To express 101P3A11 in bacterial cells, all or parts of the 101P3A11 cDNA protein coding sequence are cloned into the pET family of vectors (Novagen, Madison, WI). These vectors allow tightly controlled expression of recombinant 101P3A11 protein in bacteria with and without fusion to proteins that enhance solubility, such as NusA and thioredoxin (Trx), and epitope tags, such as 6X His (SEQ ID NO: 1402) and S-Tag™ that aid purification and detection of the recombinant protein. For example, constructs are made utilizing pET NusA fusion system 43.1 such that regions of the 101P3A11 protein are expressed as amino-terminal fusions to NusA.--

Please replace the paragraph beginning at page 88, line 19, with the following rewritten paragraph:

--pcDNA4/HisMax Constructs: To express 101P3A11 in mammalian cells, the 101P3A11 ORF was cloned into pcDNA4/HisMax Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter and the SP16 translational enhancer. The recombinant protein has Xpress™ and six histidine (6X His) (SEQ ID NO: 1402) epitopes fused to the amino-terminus. The pcDNA4/HisMax vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability along with the SV40 origin for episomal replication and simple vector rescue in cell lines expressing the large T antigen. The Zeocin resistance gene allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*.--

Please replace the paragraph beginning at page 88, line 28, with the following rewritten paragraph:

--pcDNA3.1/MycHis Constructs: To express 101P3A11 in mammalian cells, the 101P3A11 ORF, with a consensus Kozak translation initiation site, was cloned into pcDNA3.1/MycHis Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter. The recombinant proteins have the myc epitope and 6X His (SEQ ID NO: 1402) epitope fused to the carboxyl-terminus. The pcDNA3.1/MycHis vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability, along with the SV40 origin for episomal replication and

simple vector rescue in cell lines expressing the large T antigen. The Neomycin resistance gene can be used, as it allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*.--

Please replace the paragraph beginning at page 89, line 16, with the following rewritten paragraph:

--**PAPtag:** The 101P3A11 ORF, or portions thereof, of 101P3A11 are cloned into pAPtag-5 (GenHunter Corp. Nashville, TN). This construct generates an alkaline phosphatase fusion at the carboxyl-terminus of the 101P3A11 proteins while fusing the IgGκ signal sequence to the amino-terminus. Constructs are also generated in which alkaline phosphatase with an amino-terminal IgGκ signal sequence is fused to the amino-terminus of 101P3A11 proteins. The resulting recombinant 101P3A11 proteins are optimized for secretion into the media of transfected mammalian cells and can be used to identify proteins such as ligands or receptors that interact with the 101P3A11 proteins. Protein expression is driven from the CMV promoter and the recombinant proteins also contain myc and 6X His (SEQ ID NO: 1402) epitopes fused at the carboxyl-terminus that facilitates detection and purification. The Zeocin resistance gene present in the vector allows for selection of mammalian cells expressing the recombinant protein and the ampicillin resistance gene permits selection of the plasmid in *E. coli*.--

Please replace the paragraph beginning at page 89, line 27, with the following rewritten paragraph:

--**ptag5:** The 101P3A11 ORF, or portions thereof, of 101P3A11 are cloned into pTag-5. This vector is similar to pAPtag but without the alkaline phosphatase fusion. This construct generated 101P3A11 protein with an amino-terminal IgGκ signal sequence and myc and 6X His (SEQ ID NO: 1402) epitope tags at the carboxyl-terminus that facilitate detection and affinity purification. The resulting recombinant 101P3A11 protein was optimized for secretion into the media of transfected mammalian cells, and was used as immunogen or ligand to identify proteins such as ligands or receptors that interact with the 101P3A11 proteins. Protein expression is driven from the CMV promoter. The Zeocin resistance gene present in the vector allows for

selection of mammalian cells expressing the protein, and the ampicillin resistance gene permits selection of the plasmid in *E. coli*.--

Please replace the paragraph beginning at page 90, line 30, with the following rewritten paragraph:

--Additional pSR α constructs are made that fuse an epitope tag such as the FLAGTM tag to the carboxyl-terminus of 101P3A11 sequences to allow detection using anti-Flag antibodies. For example, the FLAGTM sequence 5' gat tac aag gat gac gac gat aag 3' (SEQ ID NO: 1408) is added to cloning primer at the 3' end of the ORF. Additional pSR α constructs are made to produce both amino-terminal and carboxyl-terminal GFP and myc/6X His (SEQ ID NO: 1402) fusion proteins of the full-length 101P3A11 proteins.--

Please replace the paragraph beginning at page 141, line 31, with the following rewritten paragraph:

--The generation of anti-101P3A11 polyclonal Ab (pAb) using an amino-terminal peptide encoding amino acids 1-14 (MVDPNGNESSATYF; (SEQ ID NO: 1409) as antigen was reported in our Priority Application. The effect of this antibody on 101P3A11 mediated ERK phosphorylation (Figure 38) and cAMP accumulation (Figure 39) was determined. 293T cells were transfected with control or 101P3A11 cDNA. Cells were allowed to rest overnight, and treated with anti-101P3A11 or control Ab in the presence of 0.5% or 10% FBS. Cells were lysed and analyzed by Western blotting with anti-Phospho-ERK and anti-ERK mAb. Figure 38 shows that expression of 101P3A11 induces ERK phosphorylation in cells treated with 0.5 or 10% FBS. Anti-101P3A11 pAb reduced the phosphorylation of ERK in 293T-101P3A11 cells treated with 0.5% FBS. The ERK overlay demonstrated equal loading, supporting the specificity of this data.--

Please replace Table XIX, beginning at page 186, with the following rewritten Table XIX:

--Table XIX: Motifs and Post-translational Modifications of 101P3A11

N-glycosylation site



Number of matches: 3

- 1 7-10 NESS (SEQ ID NO: 1410)
- 2 44-47 NLTI (SEQ ID NO: 1411)
- 3 90-93 NSTT (SEQ ID NO: 1412)

cAMP- and cGMP-dependent protein kinase phosphorylation site
268-271 RRDS (SEQ ID NO: 1413)

Protein kinase C phosphorylation site
266-268 SKR

Casein kinase II phosphorylation site

Number of matches: 3

- 1 56-59 SLHE (SEQ ID NO: 1414)
- 2 69-72 SGID (SEQ ID NO: 1415)
- 3 110-113 SGME (SEQ ID NO: 1416)

N-myristoylation site

Number of matches: 4

- 1 6-11 GNESSA (SEQ ID NO: 1417)
- 2 21-26 GLEEAQ (SEQ ID NO: 1418)
- 3 111-116 GMESTV (SEQ ID NO: 1419)
- 4 240-245 GTCVSH (SEQ ID NO: 1420)

G-protein coupled receptors family 1 signature

112-128 MESTVLLAMAFDRYVAI (SEQ ID NO: 1421)--

Please replace Table XXI, beginning at page 190, line 1, with the following rewritten

Table XXI:

--Table XXI: Nucleotide sequence of the splice variant (SEQ ID NO: 1422)

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1 CACATTCCTT CCATACGGTT GAGCCTCTAC CTGCCTGGTG CTGGTCACAG TTCAGCTTCT
61 TCATGATGGT GGATCCCAAT GGCAATGAAT CCAGTGCTAC ATACTTCATC CTAATAGGCC
121 TCCCTGGTTT AGAAGAGGCT CAGTTCTGGT TGGCCTCCCA TTGTGCTCCC TCTANCTATG
181 CTGTGCTAGT AATTGACAAT CATCTACATG TGCGGACGAG CACGNCGCNG AGCCCNGTAT
241 NATTCTGCNG CTTCAGCATG ACACCCTNCA GTCTCAGCCA AAGNGCATCT CNGTCAATCA
301 NACACNTGAG CTGTCGTACG AGTTGCATCA TCCTANGGCA GGATCAATGT GCGGNAGGCN
361 TGACGCAGTG CACGTACCAT GGCAGCAAGA CAGGGCCGGT ACAAATGGGG GCGAGNCGGG
421 GTGAAGATGN ACCCTCGGGT CANAGAGTGC CTCTGCGCCA AAACCTCCAT CATGNNAACA
481 GNGTATAACG GCGNAGAATC GGNNANGCGC AAGGCTAAGG AAANNCCCCA NNCNGGTACT
541 TTAACCCNGC AAANGGCANC NAAACGGGNG GGTNANTGAA CAAGGAAGGN NTGNAACTGG
601 GCCAAAACGG GNTGGGCAAN NNAAGGACTC ATGGGNCCAA GGGACGGNAA AAGGGGNAAN
661 CGGGGCGAAA TGNNAAAAC CGGGNCCCGG GGAANAANGA AGGGGAANAN GNGTGAAGGA
721 CNGGGTTCAA GGGAAAAGNA AAACCANGGG NNAGAAACCN TTCNAANGGC CCGGGNANGA

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781 AAGGAANTNN GNNNGGNGAA AAAATCNAAG AAAAGCNGNG GCNNAAAAAN GGGGGGAANN
 841 NAAANACCNN GGNCGNNAAG AACNNAANG NGGGGGGANT ANACACGGAA ANNNANGGGC
 901 GNNNAAGGGA AATAANNCGG GAACNAAAGN GCAAACCGNA CGGNAGGAAC GAAACCCACC
 961 GGAGNCGCNN AACGCCNNNC NNANCCCGAG CNGAGGTNG--

Please replace Table XXII, beginning at page 190, line 38, with the following rewritten

Table XXII:

--Table XXII: Nucleotide sequence alignment of 101P3A11 with the splice variant.

Score = 337 bits (175), Expect = 4e-89

Identities = 215/223 (96%), Gaps = 6/223 (2%)

Strand = Plus / Plus

101P3A11: 68 cacattccttccatacgggttgagcctctacctgctggtgctgggtcacagttcagcttct 127
 (SEQ ID NO: 1423)

Variant : 1 cacattccttccatacgggttgagcctctacctgctggtgctgggtcacagttcagcttct 60
 (SEQ ID NO: 1424)

101P3A11: 128 tcatgatggtggatcccaatggcaatgaatccagtgtacatacttcattcctaataaggcc 187
 (SEQ ID NO: 1423)

Variant : 61 tcatgatggtggatcccaatggcaatgaatccagtgtacatacttcattcctaataaggcc 120

101P3A11: 188 tccctggtttagaagagggtcagttctggttgcccttccattgtgctccctctacctta 247
 (SEQ ID NO: 1423)

Variant : 121 tccctggtttagaagagggtcagttctggttgcc-tccattgtgctccctctacct-- 177

101P3A11: 248 ttgctgtgctaggttaacttgacaatcatctacattgtgcggac 290
 (SEQ ID NO: 1423)

Variant : 178 atgctgtgcta-gtaa-ttgacaatcatctaca-tgtgcggac 217--

Please replace Table XXIII, beginning at page 191, line 8, with the following rewritten

Table XXIII:

--Table XXIII: Longest single amino acid sequence alignment of 101P3A11 and the splice variant.

Score = 134 bits (287), Expect (2) = 3e-29

Identities = 51/51 (100%)

Frame = +1 / +3

101P3A11: 70 HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLA 222
 (SEQ ID NO: 1425)

Variant : 3 HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLA 155
 (SEQ ID NO: 1426)--

Please replace Table XXIV, beginning at page 191, line 16, with the following rewritten

Table XXIV:

--Table XXIV: Peptide sequences from the translation of the nucleotide sequence of the splice variant .

Open reading frame	Amino acid sequences
Frame 1 (SEQ ID NO: 1427)	HIPSIRLSLYLPAGHSSASS*WWIPMAMNPVLHTSS**ASLV*KRLSSGWPPIVLPLXM LC**LTIIYMCGRARRXAXYXSAASA*HPXVSAKXHLXQSXT*AVVRVASSXGRINVRXA *RSARTMAARQGRYKWXGRXGVKMXPRVXECLCAKTSIMXTXNGXESXXRKAKEXPXXGT LTXQXAXKRXGX*TRKXXNWAKTGWAXXGLMGPDRGKRGXRGEMXKTGXRGXXKGXXXEG XGSREKXNXGXETXXXARXXKEXXXXXKSKSXGXKXGGXXXPXXXKNXXXGXTRKXXG XXGK*XGNXXANRTXGKTPTGXAXRXXXPEXR
Frame 2 (SEQ ID NO: 1428)	TFLPYG*ASTCLVLVTVQLLHDGGSQWQ*IQCYILHPNRPPWFRRGSVLVGLPLCSLXLC CASN*QSSTCADEHXAEPXXILXLQHDTLQSQPKXISVNXTXELSYELHHPXAGSMCGRX DAVHVPWQQDRAGTNGGEXG*RTLGSXSASAPKPPSXXQXITAXNRXXARLRKXPXXVL *PXKXXNGXVXEQGRXXTGPKRXGQXKDSWXQGTXXKGXXGAKXXKPGPGEXXRGXXVKD XVQGXKTXGXKPFXXPGXERXXXXXKNXKKAXAXKXGEXKXXGRXKTXXGGXXHGXXXA XKGNXXGTXKQTXRXERNPPEXXNAXXXPSXG
Frame 3 (SEQ ID NO: 1429)	HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLASHCAPSXYA VLVIDNHLHVRTSTXXSPVXFCXFSMTXSLSQXASXSIXHXSCRTSCIILXQDQCAXGX TQCTYHGSKTGPVQMGAXRGEDXPSGXRVPRLRQNLHHXNXV*RRRIGXAQG*GXXQXXYF NPAXGXXTGXXNKEGXXLGQNGXGXRTXGXXKGRXKXGXGRNXKNRXPGXEGEXX*RT GFKGKXKPxRXNXSGPGXKXGXGEXKIXKXKXKXGGXXTXXXKXKXGGXXTEXXGR XREIXREXXKXKXGRNETHRXRXTXXXXRAEV

Note: Frame 3 gives the longest subsequence that is identical with 101P3A11 amino acid sequence. In this Table each (*) indicates the product of a single stop codon, and 'X' indicates a single unknown amino acid.--

Please replace Table XXVI, beginning at page 193, line 1, with the following rewritten

Table XXVI:

--Table XXVI:

HLA Class I Nonamers (SEQ ID NOS 1430-1462, respectively in order of appearance)

HLA-A1 nonomers											
	Pos	1	2	3	4	5	6	7	8	9	score
1	245	H	V	C	A	V	F	I	F	Y	24
2	29	L	A	F	P	L	C	S	L	Y	21
3	41	V	L	G	N	L	T	I	I	Y	21
4	285	P	P	V	L	N	P	I	V	Y	20
5	111	G	M	E	S	T	V	L	L	A	19
6	117	L	L	A	M	A	F	D	R	Y	19
7	172	R	S	N	I	L	S	H	S	Y	19
8	192	D	D	I	R	V	N	V	V	Y	19
9	212	D	S	L	L	I	S	F	S	Y	19
10	57	L	H	E	P	M	Y	I	F	L	18
11	22	L	E	E	A	Q	F	W	L	A	17
12	9	S	S	A	T	Y	F	I	L	I	16
13	52	R	T	E	H	S	L	H	E	P	16

HLA-A1 nonomers

	Pos	1	2	3	4	5	6	7	8	9	score
14	54	E	H	S	L	H	E	P	M	Y	16
15	78	S	S	M	P	K	M	L	A	I	16
16	95	Q	F	D	A	C	L	L	Q	I	16
17	159	A	P	L	P	V	F	I	K	Q	16
18	183	H	Q	D	V	M	K	L	A	C	16
19	1	M	V	D	P	N	G	N	E	S	15
20	5	N	G	N	E	S	S	A	T	Y	15
21	210	G	L	D	S	L	L	I	S	F	15
22	273	L	P	V	I	L	A	N	I	Y	15
23	271	S	P	L	P	V	I	L	A	N	14
24	91	S	T	T	I	Q	F	D	A	C	13
25	121	A	F	D	R	Y	V	A	I	C	13
26	138	L	T	L	P	R	V	T	K	I	13
27	218	F	S	Y	L	L	I	L	K	T	13
28	282	L	L	V	P	P	V	L	N	P	13
29	190	A	C	D	D	I	R	V	N	V	12
30	191	C	D	D	I	R	V	N	V	V	12
31	231	T	R	E	A	Q	A	K	A	F	12
32	268	R	R	D	S	P	L	P	V	I	12
33	270	D	S	P	L	P	V	I	L	A	12

HLA-A*0201 nonomers (SEQ ID
NOS 1463-1569, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	287	V	L	N	P	I	V	Y	G	V	30
2	14	F	I	L	I	G	L	P	G	L	29
3	28	W	L	A	F	P	L	C	S	L	28
4	37	Y	L	I	A	V	L	G	N	L	28
5	222	L	I	L	K	T	V	L	G	L	28
6	66	C	M	L	S	G	I	D	I	L	26
7	108	S	L	S	G	M	E	S	T	V	26
8	181	C	L	H	Q	D	V	M	K	L	26
9	201	G	L	I	V	I	I	S	A	I	26
10	214	L	L	I	S	F	S	Y	L	L	26
11	275	V	I	L	A	N	I	Y	L	L	26
12	157	L	M	A	P	L	P	V	F	I	25
13	220	Y	L	L	I	L	K	T	V	L	25
14	276	I	L	A	N	I	Y	L	L	V	25
15	279	N	I	Y	L	L	V	P	P	V	25
16	138	L	T	L	P	R	V	T	K	I	24
17	213	S	L	L	I	S	F	S	Y	L	24
18	49	Y	I	V	R	T	E	H	S	L	23
19	143	V	T	K	I	G	V	A	A	V	23
20	188	K	L	A	C	D	D	I	R	V	23
21	198	V	V	Y	G	L	I	V	I	I	23
22	21	G	L	E	E	A	Q	F	W	L	22
23	40	A	V	L	G	N	L	T	I	I	22
24	206	I	S	A	I	G	L	D	S	L	22
25	11	A	T	Y	F	I	L	I	G	L	21
26	60	P	M	Y	I	F	L	C	M	L	21

HLA-A*0201 nonomers (SEQ ID
NOS 1463-1569, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
27	135	A	T	V	L	T	<u>L</u>	P	R	V	21
28	160	P	L	P	V	F	<u>I</u>	K	Q	L	21
29	174	N	I	L	S	H	<u>S</u>	Y	C	L	21
30	207	S	A	I	G	L	<u>D</u>	S	L	L	21
31	272	P	L	P	V	I	<u>L</u>	A	N	I	21
32	283	L	V	P	P	V	<u>L</u>	N	P	I	21
33	67	M	L	S	G	I	<u>D</u>	I	L	I	20
34	101	L	<u>Q</u>	I	F	A	<u>I</u>	H	S	L	20
35	282	L	L	V	P	P	<u>V</u>	L	N	P	20
36	299	E	I	R	Q	R	<u>I</u>	L	R	L	20
37	304	I	L	R	L	F	<u>H</u>	V	A	T	20
38	39	I	A	V	L	G	<u>N</u>	L	T	I	19
39	45	L	T	I	I	Y	<u>I</u>	V	R	T	19
40	92	T	T	I	Q	F	<u>D</u>	A	C	L	19
41	110	S	G	M	E	S	<u>T</u>	V	L	L	19
42	127	A	I	C	H	P	<u>L</u>	R	H	A	19
43	132	L	R	H	A	T	<u>V</u>	L	T	L	19
44	149	A	A	V	V	R	<u>G</u>	A	A	L	19
45	155	A	A	L	M	A	<u>P</u>	L	P	V	19
46	156	A	L	M	A	P	<u>L</u>	P	V	F	19
47	203	I	V	I	I	S	<u>A</u>	I	G	L	19
48	208	A	I	G	L	D	<u>S</u>	L	L	I	19
49	216	I	S	F	S	Y	<u>L</u>	L	I	L	19
50	219	S	Y	L	L	I	<u>L</u>	K	T	V	19
51	221	L	L	I	L	K	<u>T</u>	V	L	G	19
52	223	I	L	K	T	V	<u>L</u>	G	L	T	19
53	17	I	G	L	P	G	<u>L</u>	E	E	A	18
54	33	L	C	S	L	Y	<u>L</u>	I	A	V	18
55	34	C	S	L	Y	L	<u>I</u>	A	V	L	18
56	38	L	I	A	V	L	<u>G</u>	N	L	T	18
57	43	G	N	L	T	I	<u>I</u>	Y	I	V	18
58	85	A	I	F	W	F	<u>N</u>	S	T	T	18
59	118	L	A	M	A	F	<u>D</u>	R	Y	V	18
60	194	I	R	V	N	V	<u>V</u>	Y	G	L	18
61	210	G	L	D	S	L	<u>L</u>	I	S	F	18
62	215	L	I	S	F	S	<u>Y</u>	L	L	I	18
63	246	V	C	A	V	F	<u>I</u>	F	Y	V	18
64	254	V	P	F	I	G	<u>L</u>	S	M	V	18
65	15	I	L	I	G	L	<u>P</u>	G	L	E	17
66	63	I	F	L	C	M	<u>L</u>	S	G	I	17
67	72	D	I	L	I	S	<u>T</u>	S	S	M	17
68	93	T	I	Q	F	D	<u>A</u>	C	L	L	17
69	98	A	C	L	L	Q	<u>I</u>	F	A	I	17
70	111	G	M	E	S	T	<u>V</u>	L	L	A	17
71	120	M	A	F	D	R	<u>Y</u>	V	A	I	17
72	167	Q	L	P	F	C	<u>R</u>	S	N	I	17
73	197	N	V	V	Y	G	<u>L</u>	I	V	I	17
74	226	T	V	L	G	L	<u>T</u>	R	E	A	17
75	281	Y	L	L	V	P	<u>P</u>	V	L	N	17

HLA-A*0201 nonomers (SEQ ID
NOS 1463-1569, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
76	31	F	P	L	C	S	<u>L</u>	Y	L	I	16
77	56	S	L	H	E	P	<u>M</u>	Y	I	F	16
78	70	G	I	D	I	L	<u>I</u>	S	T	S	16
79	78	S	S	M	P	K	<u>M</u>	L	A	I	16
80	79	S	M	P	K	M	<u>L</u>	A	I	F	16
81	104	F	A	I	H	S	<u>L</u>	S	G	M	16
82	119	A	M	A	F	D	<u>R</u>	Y	V	A	16
83	144	T	K	I	G	V	<u>A</u>	A	V	V	16
84	147	G	V	A	A	V	<u>V</u>	R	G	A	16
85	186	V	M	K	L	A	<u>C</u>	D	D	I	16
86	230	L	T	R	E	A	<u>Q</u>	A	K	A	16
87	238	A	F	G	T	C	<u>V</u>	S	H	V	16
88	249	V	F	I	F	Y	<u>V</u>	P	F	I	16
89	302	Q	R	I	L	R	<u>L</u>	F	H	V	16
90	303	R	I	L	R	L	<u>F</u>	H	V	A	16
91	18	G	L	P	G	L	<u>E</u>	E	A	Q	15
92	35	S	L	Y	L	I	<u>A</u>	V	L	G	15
93	42	L	G	N	L	T	<u>I</u>	I	Y	I	15
94	46	T	I	I	Y	I	<u>V</u>	R	T	E	15
95	69	S	G	I	D	I	<u>L</u>	I	S	T	15
96	76	S	T	S	S	M	<u>P</u>	K	M	L	15
97	131	P	L	R	H	A	<u>T</u>	V	L	T	15
98	137	V	L	T	L	P	<u>R</u>	V	T	K	15
99	153	R	G	A	A	L	<u>M</u>	A	P	L	15
100	190	A	C	D	D	I	<u>R</u>	V	N	V	15
101	191	C	D	D	I	R	<u>V</u>	N	V	V	15
102	204	V	I	I	S	A	<u>I</u>	G	L	D	15
103	241	T	C	V	S	H	<u>V</u>	C	A	V	15
104	251	I	F	Y	V	P	<u>F</u>	I	G	L	15
105	269	R	D	S	P	L	<u>P</u>	V	I	L	15
106	280	I	Y	L	L	V	<u>P</u>	P	V	L	15
107	306	R	L	F	H	V	<u>A</u>	T	H	A	15

HLA A*0203 nonomers (SEQ ID
NOS 1570-1594, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	148	V	<u>A</u>	A	V	V	R	<u>G</u>	A	A	14
2	119	A	<u>M</u>	A	F	D	R	<u>Y</u>	V	A	13
3	147	G	<u>V</u>	A	A	V	V	R	G	A	12
4	97	D	<u>A</u>	C	L	L	Q	<u>I</u>	F	A	11
5	127	A	<u>I</u>	C	H	P	L	<u>R</u>	H	A	10
6	3	D	<u>P</u>	N	G	N	E	<u>S</u>	S	A	9
7	17	I	<u>G</u>	L	P	G	L	<u>E</u>	E	A	9
8	22	L	<u>E</u>	E	A	Q	F	<u>W</u>	L	A	9
9	32	P	<u>L</u>	C	S	L	Y	<u>L</u>	I	A	9
10	77	T	<u>S</u>	S	M	P	K	<u>M</u>	L	A	9
11	90	N	<u>S</u>	T	T	I	Q	<u>F</u>	D	A	9

HLA A*0203 nonomers (SEQ ID
NOS 1570-1594, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
12	111	G	M	E	S	T	V	L	L	A	9
13	113	E	S	T	V	L	L	A	M	A	9
14	141	P	R	V	T	K	I	G	V	A	9
15	142	R	V	T	K	I	G	V	A	A	9
16	151	V	V	R	G	A	A	L	M	A	9
17	182	L	H	Q	D	V	M	K	L	A	9
18	200	Y	G	L	I	V	I	I	S	A	9
19	226	T	V	L	G	L	T	R	E	A	9
20	228	L	G	L	T	R	E	A	Q	A	9
21	230	L	T	R	E	A	Q	A	K	A	9
22	240	G	T	C	V	S	H	V	C	A	9
23	270	D	S	P	L	P	V	I	L	A	9
24	303	R	I	L	R	L	F	H	V	A	9
25	306	R	L	F	H	V	A	T	H	A	9

HLA-A26 nonomers (SEQ ID NOS
1595-1675, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	299	E	I	R	Q	R	I	L	R	L	30
2	72	D	I	L	I	S	T	S	S	M	27
3	248	A	V	F	I	F	Y	V	P	F	27
4	210	G	L	D	S	L	L	I	S	F	26
5	14	F	I	L	I	G	L	P	G	L	24
6	56	S	L	H	E	P	M	Y	I	F	24
7	117	L	L	A	M	A	F	D	R	Y	24
8	222	L	I	L	K	T	V	L	G	L	24
9	245	H	V	C	A	V	F	I	F	Y	24
10	11	A	T	Y	F	I	L	I	G	L	23
11	37	Y	L	I	A	V	L	G	N	L	23
12	114	S	T	V	L	L	A	M	A	F	23
13	156	A	L	M	A	P	L	P	V	F	23
14	162	P	V	F	I	K	Q	L	P	F	23
15	181	C	L	H	Q	D	V	M	K	L	23
16	28	W	L	A	F	P	L	C	S	L	22
17	92	T	T	I	Q	F	D	A	C	L	22
18	160	P	L	P	V	F	I	K	Q	L	22
19	203	I	V	I	I	S	A	I	G	L	22
20	213	S	L	L	I	S	F	S	Y	L	22
21	275	V	I	L	A	N	I	Y	L	L	22
22	193	D	I	R	V	N	V	V	Y	G	21
23	242	C	V	S	H	V	C	A	V	F	21
24	76	S	T	S	S	M	P	K	M	L	20
25	253	Y	V	P	F	I	G	L	S	M	20
26	274	P	V	I	L	A	N	I	Y	L	20
27	23	E	E	A	Q	F	W	L	A	F	19
28	41	V	L	G	N	L	T	I	I	Y	19
29	49	Y	I	V	R	T	E	H	S	L	19

HLA-A26 nonomers (SEQ ID NOS
1595-1675, respectively in
order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
30	150	A V V R G A A L M	19
31	174	N I L S H S Y C L	19
32	192	D D I R V N V V Y	19
33	214	L L I S F S Y L L	19
34	251	I F Y V P F I G L	19
35	8	E S S A T Y F I L	18
36	21	G L E E A Q F W L	18
37	45	L T I I Y I V R T	18
38	54	E H S L H E P M Y	18
39	59	E P M Y I F L C M	18
40	88	W F N S T T I Q F	18
41	93	T I Q F D A C L L	18
42	185	D V M K L A C D D	18
43	198	V V Y G L I V I I	18
44	62	Y I F L C M L S G	17
45	70	G I D I L I S T S	17
46	79	S M P K M L A I F	17
47	96	F D A C L L Q I F	17
48	104	F A I H S L S G M	17
49	138	L T L P R V T K I	17
50	143	V T K I G V A A V	17
51	204	V I I S A I G L D	17
52	212	D S L L I S F S Y	17
53	220	Y L L I L K T V L	17
54	256	F I G L S M V H R	17
55	283	L V P P V L N P I	17
56	29	L A F P L C S L Y	16
57	40	A V L G N L T I I	16
58	46	T I I Y I V R T E	16
59	52	R T E H S L H E P	16
60	75	I S T S S M P K M	16
61	91	S T T I Q F D A C	16
62	135	A T V L T L P R V	16
63	147	G V A A V V R G A	16
64	201	G L I V I I S A I	16
65	257	I G L S M V H R F	16
66	279	N I Y L L V P P V	16
67	30	A F P L C S L Y L	15
68	101	L Q I F A I H S L	15
69	115	T V L L A M A F D	15
70	127	A I C H P L R H A	15
71	153	R G A A L M A P L	15
72	163	V F I K Q L P F C	15
73	215	L I S F S Y L L I	15
74	216	I S F S Y L L I L	15
75	225	K T V L G L T R E	15
76	272	P L P V I L A N I	15
77	282	L L V P P V L N P	15
78	286	P V L N P I V Y G	15

HLA-A26 nonomers (SEQ ID NOS
1595-1675, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
79	287	V	L	N	P	I	V	Y	G	V	15
80	296	K	T	K	E	I	R	Q	R	I	15
81	303	R	I	L	R	L	F	H	V	A	15

HLA-A3 nonomers (SEQ ID NOS
1676-1747, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	137	V	L	<u>T</u>	L	P	<u>R</u>	<u>V</u>	T	K	30
2	229	G	L	<u>T</u>	R	E	<u>A</u>	<u>Q</u>	A	K	27
3	145	K	I	<u>G</u>	V	A	<u>A</u>	<u>V</u>	V	R	26
4	150	A	V	<u>V</u>	R	G	<u>A</u>	<u>A</u>	L	M	24
5	290	P	I	<u>V</u>	Y	G	<u>V</u>	<u>K</u>	T	K	24
6	35	S	L	<u>Y</u>	L	I	<u>A</u>	<u>V</u>	L	G	23
7	156	A	L	<u>M</u>	A	P	<u>L</u>	<u>P</u>	V	F	23
8	47	I	I	<u>Y</u>	I	V	<u>R</u>	<u>T</u>	E	H	22
9	50	I	V	<u>R</u>	T	E	<u>H</u>	<u>S</u>	L	H	22
10	142	R	V	<u>T</u>	K	I	<u>G</u>	<u>V</u>	A	A	22
11	151	V	V	<u>R</u>	G	A	<u>A</u>	<u>L</u>	M	A	22
12	242	C	V	<u>S</u>	H	V	<u>C</u>	<u>A</u>	V	F	22
13	248	A	V	<u>F</u>	I	F	<u>Y</u>	<u>V</u>	P	F	22
14	116	V	L	<u>L</u>	A	M	<u>A</u>	<u>F</u>	D	R	21
15	192	D	D	<u>I</u>	R	V	<u>N</u>	<u>V</u>	V	Y	21
16	303	R	I	<u>L</u>	R	L	<u>F</u>	<u>H</u>	V	A	21
17	304	I	L	<u>R</u>	L	F	<u>H</u>	<u>V</u>	A	T	21
18	108	S	L	<u>S</u>	G	M	<u>E</u>	<u>S</u>	T	V	20
19	198	V	V	<u>Y</u>	G	L	<u>I</u>	<u>V</u>	I	I	20
20	291	I	V	<u>Y</u>	G	V	<u>K</u>	<u>T</u>	K	E	20
21	15	I	L	<u>I</u>	G	L	<u>P</u>	<u>G</u>	L	E	19
22	44	N	L	<u>T</u>	I	I	<u>Y</u>	<u>I</u>	V	R	19
23	73	I	L	<u>I</u>	S	T	<u>S</u>	<u>S</u>	M	P	19
24	74	L	I	<u>S</u>	T	S	<u>S</u>	<u>M</u>	P	K	19
25	99	C	L	<u>L</u>	Q	I	<u>F</u>	<u>A</u>	I	H	19
26	162	P	V	<u>F</u>	I	K	<u>Q</u>	<u>L</u>	P	F	19
27	203	I	V	<u>I</u>	I	S	<u>A</u>	<u>I</u>	G	L	19
28	221	L	L	<u>I</u>	L	K	<u>T</u>	<u>V</u>	L	G	19
29	245	H	V	<u>C</u>	A	V	<u>F</u>	<u>I</u>	F	Y	19
30	306	R	L	<u>F</u>	H	V	<u>A</u>	<u>T</u>	H	A	19
31	40	A	V	<u>L</u>	G	N	<u>L</u>	<u>T</u>	I	I	18
32	85	A	I	<u>F</u>	W	F	<u>N</u>	<u>S</u>	T	T	18
33	205	I	I	<u>S</u>	A	I	<u>G</u>	<u>L</u>	D	S	18
34	220	Y	L	<u>L</u>	I	L	<u>K</u>	<u>T</u>	V	L	18
35	253	Y	V	<u>P</u>	F	I	<u>G</u>	<u>L</u>	S	M	18
36	37	Y	L	<u>I</u>	A	V	<u>L</u>	<u>G</u>	N	L	17
37	41	V	L	<u>G</u>	N	L	<u>T</u>	<u>I</u>	I	Y	17
38	117	L	L	<u>A</u>	M	A	<u>F</u>	<u>D</u>	R	Y	17
39	131	P	L	<u>R</u>	H	A	<u>T</u>	<u>V</u>	L	T	17
40	136	T	V	<u>L</u>	T	L	<u>P</u>	<u>R</u>	V	T	17

HLA-A3 nonomers (SEQ ID NOS
1676-1747, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
41	180	Y	C	<u>L</u>	H	Q	<u>D</u>	<u>V</u>	M	K	17
42	201	G	<u>L</u>	<u>I</u>	V	I	<u>I</u>	S	A	I	17
43	213	S	<u>L</u>	<u>L</u>	I	S	<u>F</u>	<u>S</u>	Y	L	17
44	256	F	I	<u>G</u>	L	S	<u>M</u>	<u>V</u>	H	R	17
45	261	M	<u>V</u>	<u>H</u>	R	F	<u>S</u>	<u>K</u>	R	R	17
46	276	I	<u>L</u>	<u>A</u>	N	I	<u>Y</u>	<u>L</u>	L	V	17
47	281	Y	<u>L</u>	<u>L</u>	V	P	<u>P</u>	<u>V</u>	L	N	17
48	286	P	<u>V</u>	<u>L</u>	N	P	<u>I</u>	<u>V</u>	Y	G	17
49	288	L	<u>N</u>	<u>P</u>	I	V	<u>Y</u>	<u>G</u>	V	K	17
50	309	H	<u>V</u>	<u>A</u>	T	H	<u>A</u>	S	E	P	17
51	1	M	<u>V</u>	<u>D</u>	P	N	<u>G</u>	N	E	S	16
52	56	S	<u>L</u>	<u>H</u>	E	P	<u>M</u>	<u>Y</u>	I	F	16
53	70	G	<u>I</u>	<u>D</u>	I	L	<u>I</u>	S	T	S	16
54	72	D	<u>I</u>	<u>L</u>	I	S	<u>T</u>	S	S	M	16
55	115	T	<u>V</u>	<u>L</u>	L	A	<u>M</u>	<u>A</u>	F	D	16
56	125	Y	<u>V</u>	<u>A</u>	I	C	<u>H</u>	<u>P</u>	L	R	16
57	144	T	<u>K</u>	<u>I</u>	G	V	<u>A</u>	<u>A</u>	V	V	16
58	167	Q	<u>L</u>	<u>P</u>	F	C	R	S	N	I	16
59	175	I	<u>L</u>	<u>S</u>	H	S	<u>Y</u>	<u>C</u>	L	H	16
60	195	R	<u>V</u>	<u>N</u>	V	V	<u>Y</u>	<u>G</u>	L	I	16
61	197	N	<u>V</u>	<u>V</u>	Y	G	<u>L</u>	<u>I</u>	V	I	16
62	210	G	<u>L</u>	<u>D</u>	S	L	<u>L</u>	<u>I</u>	S	F	16
63	282	L	<u>L</u>	<u>V</u>	P	P	<u>V</u>	<u>L</u>	N	P	16
64	299	E	<u>I</u>	<u>R</u>	Q	R	<u>I</u>	<u>L</u>	R	L	16
65	301	R	<u>Q</u>	<u>R</u>	I	L	<u>R</u>	<u>L</u>	F	H	16
66	16	L	<u>I</u>	<u>G</u>	L	P	<u>G</u>	<u>L</u>	E	E	15
67	46	T	<u>I</u>	<u>I</u>	Y	I	<u>V</u>	<u>R</u>	T	E	15
68	102	Q	<u>I</u>	<u>F</u>	A	I	<u>H</u>	<u>S</u>	L	S	15
69	193	D	<u>I</u>	<u>R</u>	V	N	<u>V</u>	<u>V</u>	Y	G	15
70	208	A	<u>I</u>	<u>G</u>	L	D	<u>S</u>	<u>L</u>	L	I	15
71	223	I	<u>L</u>	<u>K</u>	T	V	<u>L</u>	<u>G</u>	L	T	15
72	237	K	<u>A</u>	<u>F</u>	G	T	<u>C</u>	<u>V</u>	S	H	15

HLA-B*0702 nonomers (SEQ ID
NOS 1748-1812, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	130	H	<u>P</u>	L	R	H	A	T	V	L	22
2	59	E	<u>P</u>	<u>M</u>	Y	I	F	L	C	M	21
3	168	L	<u>P</u>	F	C	R	S	N	I	L	20
4	289	N	<u>P</u>	I	V	Y	G	V	K	T	19
5	3	D	<u>P</u>	N	G	N	E	S	S	A	18
6	19	L	<u>P</u>	<u>G</u>	L	E	E	A	Q	F	18
7	140	L	<u>P</u>	R	V	T	K	I	G	V	18
8	284	V	<u>P</u>	<u>P</u>	V	L	N	P	I	V	17
9	31	F	<u>P</u>	L	C	S	L	Y	L	I	16
10	254	V	<u>P</u>	F	I	G	L	S	M	V	16
11	269	R	<u>D</u>	S	<u>P</u>	L	<u>P</u>	<u>V</u>	I	L	16

HLA-B*0702 nonomers (SEQ ID
NOS 1748-1812, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
12	149	A A V V R G A A L	15
13	153	R G A A L M A P L	15
14	156	A L M A P L P V F	15
15	251	I F Y V P F I G L	15
16	299	E I R Q R I L R L	15
17	8	E S S A T Y F I L	14
18	28	W L A F P L C S L	14
19	30	A F P L C S L Y L	14
20	110	S G M E S T V L L	14
21	132	L R H A T V L T L	14
22	159	A P L P V F I K Q	14
23	222	L I L K T V L G L	14
24	271	S P L P V I L A N	14
25	25	A Q F W L A F P L	13
26	109	L S G M E S T V L	13
27	124	R Y V A I C H P L	13
28	216	I S F S Y L L I L	13
29	268	R R D S P L P V I	13
30	280	I Y L L V P P V L	13
31	11	A T Y F I L I G L	12
32	34	C S L Y L I A V L	12
33	57	L H E P M Y I F L	12
34	76	S T S S M P K M L	12
35	142	R V T K I G V A A	12
36	151	V V R G A A L M A	12
37	190	A C D D I R V N V	12
38	194	I R V N V V Y G L	12
39	206	I S A I G L D S L	12
40	207	S A I G L D S L L	12
41	220	Y L L I L K T V L	12
42	267	K R R D S P L P V	12
43	304	I L R L F H V A T	12
44	14	F I L I G L P G L	11
45	23	E E A Q F W L A F	11
46	37	Y L I A V L G N L	11
47	40	A V L G N L T I I	11
48	77	T S S M P K M L A	11
49	78	S S M P K M L A I	11
50	80	M P K M L A I F W	11
51	92	T T I Q F D A C L	11
52	112	M E S T V L L A M	11
53	119	A M A F D R Y V A	11
54	127	A I C H P L R H A	11
55	131	P L R H A T V L T	11
56	155	A A L M A P L P V	11
57	157	L M A P L P V F I	11
58	181	C L H Q D V M K L	11
59	203	I V I I S A I G L	11
60	208	A I G L D S L L I	11

HLA-B*0702 nonomers(SEQ ID
NOS 1748-1812, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
61	213	S	L	L	I	S	F	S	Y	L	11
62	248	A	V	F	I	F	Y	V	P	F	11
63	265	F	S	K	R	R	D	S	P	L	11
64	275	V	I	L	A	N	I	Y	L	L	11
65	285	P	P	V	L	N	P	I	V	Y	11

HLA-B*08 nonomers(SEQ ID
NOS 1813-1847, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	299	E	I	R	Q	R	I	L	R	L	31
2	265	F	S	K	R	R	D	S	P	L	29
3	149	A	A	V	V	R	G	A	A	L	24
4	168	L	P	F	C	R	S	N	I	L	24
5	294	G	V	K	T	K	E	I	R	Q	21
6	120	M	A	F	D	R	Y	V	A	I	20
7	292	V	Y	G	V	K	T	K	E	I	20
8	21	G	L	E	E	A	Q	F	W	L	19
9	78	S	S	M	P	K	M	L	A	I	19
10	160	P	L	P	V	F	I	K	Q	L	19
11	186	V	M	K	L	A	C	D	D	I	18
12	213	S	L	L	I	S	F	S	Y	L	18
13	221	L	L	I	L	K	T	V	L	G	18
14	296	K	T	K	E	I	R	Q	R	I	18
15	297	T	K	E	I	R	Q	R	I	L	18
16	130	H	P	L	R	H	A	T	V	L	17
17	181	C	L	H	Q	D	V	M	K	L	17
18	223	I	L	K	T	V	L	G	L	T	17
19	28	W	L	A	F	P	L	C	S	L	16
20	37	Y	L	I	A	V	L	G	N	L	16
21	56	S	L	H	E	P	M	Y	I	F	16
22	80	M	P	K	M	L	A	I	F	W	16
23	162	P	V	F	I	K	Q	L	P	F	16
24	201	G	L	I	V	I	I	S	A	I	16
25	207	S	A	I	G	L	D	S	L	L	16
26	214	L	L	I	S	F	S	Y	L	L	16
27	220	Y	L	L	I	L	K	T	V	L	16
28	233	E	A	Q	A	K	A	F	G	T	16
29	275	V	I	L	A	N	I	Y	L	L	16
30	304	I	L	R	L	F	H	V	A	T	16
31	14	F	I	L	I	G	L	P	G	L	15
32	110	S	G	M	E	S	T	V	L	L	15
33	138	L	T	L	P	R	V	T	K	I	15
34	164	F	I	K	Q	L	P	F	C	R	15
35	222	L	I	L	K	T	V	L	G	L	15

HLA-B*1510 nonomers (SEQ ID
NOS 1848-1890, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	57	L	H	E	P	M	Y	I	F	L	23
2	244	S	H	V	C	A	V	F	I	F	17
3	269	R	D	S	P	L	P	V	I	L	16
4	280	I	Y	L	L	V	P	P	V	L	16
5	262	V	H	R	F	S	K	R	R	D	15
6	299	E	I	R	Q	R	I	L	R	L	15
7	106	I	H	S	L	S	G	M	E	S	14
8	206	I	S	A	I	G	L	D	S	L	14
9	220	Y	L	L	I	L	K	T	V	L	14
10	251	I	F	Y	V	P	F	I	G	L	14
11	297	T	K	E	I	R	Q	R	I	L	14
12	21	G	L	E	E	A	Q	F	W	L	13
13	34	C	S	L	Y	L	I	A	V	L	13
14	54	E	H	S	L	H	E	P	M	Y	13
15	110	S	G	M	E	S	T	V	L	L	13
16	194	I	R	V	N	V	V	Y	G	L	13
17	8	E	S	S	A	T	Y	F	I	L	12
18	14	F	I	L	I	G	L	P	G	L	12
19	28	W	L	A	F	P	L	C	S	L	12
20	66	C	M	L	S	G	I	D	I	L	12
21	76	S	T	S	S	M	P	K	M	L	12
22	92	T	T	I	Q	F	D	A	C	L	12
23	109	L	S	G	M	E	S	T	V	L	12
24	130	H	P	L	R	H	A	T	V	L	12
25	132	L	R	H	A	T	V	L	T	L	12
26	149	A	A	V	V	R	G	A	A	L	12
27	153	R	G	A	A	L	M	A	P	L	12
28	160	P	L	P	V	F	I	K	Q	L	12
29	181	C	L	H	Q	D	V	M	K	L	12
30	182	L	H	Q	D	V	M	K	L	A	12
31	203	I	V	I	I	S	A	I	G	L	12
32	216	I	S	F	S	Y	L	L	I	L	12
33	222	L	I	L	K	T	V	L	G	L	12
34	275	V	I	L	A	N	I	Y	L	L	12
35	37	Y	L	I	A	V	L	G	N	L	11
36	49	Y	I	V	R	T	E	H	S	L	11
37	93	T	I	Q	F	D	A	C	L	L	11
38	101	L	Q	I	F	A	I	H	S	L	11
39	129	C	H	P	L	R	H	A	T	V	11
40	133	R	H	A	T	V	L	T	L	P	11
41	177	S	H	S	Y	C	L	H	Q	D	11
42	207	S	A	I	G	L	D	S	L	L	11
43	257	I	G	L	S	M	V	H	R	F	11

HLA-B*2705 nonomers (SEQ ID
NOS 1891-2008, respectively
in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	score
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HLA-B*2705 nonomers (SEQ ID
NOS 1891-2008, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
1	194	I R V N V V Y G L	25
2	268	R R D S P L P V I	24
3	132	L R H A T V L T L	23
4	300	I R Q R I L R L F	23
5	305	L R L F H V A T H	23
6	231	T R E A Q A K A F	21
7	34	C S L Y L I A V L	18
8	299	E I R Q R I L R L	18
9	6	G N E S S A T Y F	17
10	66	C M L S G I D I L	17
11	162	P V F I K Q L P F	17
12	207	S A I G L D S L L	17
13	210	G L D S L L I S F	17
14	220	Y L L I L K T V L	17
15	237	K A F G T C V S H	17
16	269	R D S P L P V I L	17
17	280	I Y L L V P P V L	17
18	295	V K T K E I R Q R	17
19	11	A T Y F I L I G L	16
20	14	F I L I G L P G L	16
21	21	G L E E A Q F W L	16
22	25	A Q F W L A F P L	16
23	37	Y L I A V L G N L	16
24	92	T T I Q F D A C L	16
25	101	L Q I F A I H S L	16
26	124	R Y V A I C H P L	16
27	130	H P L R H A T V L	16
28	141	P R V T K I G V A	16
29	153	R G A A L M A P L	16
30	181	C L H Q D V M K L	16
31	201	G L I V I I S A I	16
32	203	I V I I S A I G L	16
33	216	I S F S Y L L I L	16
34	222	L I L K T V L G L	16
35	255	P F I G L S M V H	16
36	257	I G L S M V H R F	16
37	275	V I L A N I Y L L	16
38	47	I I Y I V R T E H	15
39	109	L S G M E S T V L	15
40	114	S T V L L A M A F	15
41	123	D R Y V A I C H P	15
42	145	K I G V A A V V R	15
43	156	A L M A P L P V F	15
44	168	L P F C R S N I L	15
45	172	R S N I L S H S Y	15
46	198	V V Y G L I V I I	15
47	206	I S A I G L D S L	15
48	229	G L T R E A Q A K	15
49	248	A V F I F Y V P F	15

HLA-B*2705 nonomers (SEQ ID
NOS 1891-2008, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
50	251	I F Y V P F I G L	15
51	274	P V I L A N I Y L	15
52	290	P I V Y G V K T K	15
53	298	K E I R Q R I L R	15
54	19	L P G L E E A Q F	14
55	29	L A F P L C S L Y	14
56	30	A F P L C S L Y L	14
57	39	I A V L G N L T I	14
58	40	A V L G N L T I I	14
59	79	S M P K M L A I F	14
60	81	P K M L A I F W F	14
61	99	C L L Q I F A I H	14
62	137	V L T L P R V T K	14
63	138	L T L P R V T K I	14
64	150	A V V R G A A L M	14
65	160	P L P V F I K Q L	14
66	174	N I L S H S Y C L	14
67	180	Y C L H Q D V M K	14
68	192	D D I R V N V V Y	14
69	212	D S L L I S F S Y	14
70	213	S L L I S F S Y L	14
71	214	L L I S F S Y L L	14
72	260	S M V H R F S K R	14
73	263	H R F S K R R D S	14
74	267	K R R D S P L P V	14
75	293	Y G V K T K E I R	14
76	301	R Q R I L R L F H	14
77	302	Q R I L R L F H V	14
78	5	N G N E S S A T Y	13
79	23	E E A Q F W L A F	13
80	28	W L A F P L C S L	13
81	44	N L T I I Y I V R	13
82	51	V R T E H S L H E	13
83	56	S L H E P M Y I F	13
84	60	P M Y I F L C M L	13
85	72	D I L I S T S S M	13
86	74	L I S T S S M P K	13
87	75	I S T S S M P K M	13
88	98	A C L L Q I F A I	13
89	104	F A I H S L S G M	13
90	110	S G M E S T V L L	13
91	116	V L L A M A F D R	13
92	126	V A I C H P L R H	13
93	149	A A V V R G A A L	13
94	158	M A P L P V F I K	13
95	164	F I K Q L P F C R	13
96	170	F C R S N I L S H	13
97	171	C R S N I L S H S	13
98	187	M K L A C D D I R	13

HLA-B*2705 nonomers (SEQ ID
NOS 1891-2008, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
99	217	S F S Y L L I L K	13
100	224	L K T V L G L T R	13
101	242	C V S H V C A V F	13
102	256	F I G L S M V H R	13
103	261	M V H R F S K R R	13
104	49	Y I V R T E H S L	12
105	57	L H E P M Y I F L	12
106	88	W F N S T T I Q F	12
107	96	F D A C L L Q I F	12
108	134	H A T V L T L P R	12
109	152	V R G A A L M A P	12
110	179	S Y C L H Q D V M	12
111	197	N V V Y G L I V I	12
112	244	S H V C A V F I F	12
113	265	F S K R R D S P L	12
114	273	L P V I L A N I Y	12
115	285	P P V L N P I V Y	12
116	288	L N P I V Y G V K	12
117	296	K T K E I R Q R I	12
118	297	T K E I R Q R I L	12

HLA-B*2709 nonomers (SEQ ID
NOS 2009-2063, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
1	194	I R V N V V Y G L	24
2	268	R R D S P L P V I	24
3	132	L R H A T V L T L	22
4	267	K R R D S P L P V	21
5	300	I R Q R I L R L F	20
6	231	T R E A Q A K A F	19
7	302	Q R I L R L F H V	19
8	124	R Y V A I C H P L	16
9	269	R D S P L P V I L	16
10	43	G N L T I I Y I V	15
11	216	I S F S Y L L I L	15
12	11	A T Y F I L I G L	14
13	25	A Q F W L A F P L	14
14	153	R G A A L M A P L	14
15	174	N I L S H S Y C L	14
16	222	L I L K T V L G L	14
17	257	I G L S M V H R F	14
18	280	I Y L L V P P V L	14
19	6	G N E S S A T Y F	13
20	14	F I L I G L P G L	13
21	21	G L E E A Q F W L	13
22	66	C M L S G I D I L	13

HLA-B*2709 nonomers (SEQ ID
NOS 2009-2063, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
23	130	H P L R H A T V L	13
24	201	G L I V I I S A I	13
25	203	I V I I S A I G L	13
26	214	L L I S F S Y L L	13
27	251	I F Y V P F I G L	13
28	263	H R F S K R R D S	13
29	275	V I L A N I Y L L	13
30	305	L R L F H V A T H	13
31	30	A F P L C S L Y L	12
32	34	C S L Y L I A V L	12
33	37	Y L I A V L G N L	12
34	51	V R T E H S L H E	12
35	60	P M Y I F L C M L	12
36	75	I S T S S M P K M	12
37	93	T I Q F D A C L L	12
38	123	D R Y V A I C H P	12
39	135	A T V L T L P R V	12
40	138	L T L P R V T K I	12
41	149	A A V V R G A A L	12
42	155	A A L M A P L P V	12
43	168	L P F C R S N I L	12
44	181	C L H Q D V M K L	12
45	188	K L A C D D I R V	12
46	190	A C D D I R V N V	12
47	195	R V N V V Y G L I	12
48	210	G L D S L L I S F	12
49	213	S L L I S F S Y L	12
50	220	Y L L I L K T V L	12
51	248	A V F I F Y V P F	12
52	279	N I Y L L V P P V	12
53	287	V L N P I V Y G V	12
54	296	K T K E I R Q R I	12
55	299	E I R Q R I L R L	12

HLA-B*5101 nonomers (SEQ ID
NOS 2064-2132, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
1	39	I A V L G N L T I	26
2	31	F P L C S L Y L I	25
3	120	M A F D R Y V A I	24
4	130	H P L R H A T V L	23
5	118	L A M A F D R Y V	22
6	140	L P R V T K I G V	22
7	155	A A L M A P L P V	22
8	42	L G N L T I I Y I	21
9	254	V P F I G L S M V	21
10	284	V P P V L N P I V	21

HLA-B*5101 nonomers (SEQ ID
NOS 2064-2132, respectively
in order of appearance)

	Pos	1 2 3 4 5 6 7 8 9	score
11	168	L P F C R S N I L	20
12	235	Q A K A F G T C V	20
13	138	L T L P R V T K I	19
14	159	A P L P V F I K Q	18
15	189	L A C D D I R V N	18
16	198	V V Y G L I V I I	18
17	277	L A N I Y L L V P	18
18	207	S A I G L D S L L	17
19	283	L V P P V L N P I	17
20	63	I F L C M L S G I	16
21	86	I F W F N S T T I	16
22	110	S G M E S T V L L	16
23	144	T K I G V A A V V	16
24	149	A A V V R G A A L	16
25	197	N V V Y G L I V I	16
26	271	S P L P V I L A N	16
27	280	I Y L L V P P V L	16
28	3	D P N G N E S S A	15
29	40	A V L G N L T I I	15
30	97	D A C L L Q I F A	15
31	132	L R H A T V L T L	15
32	222	L I L K T V L G L	15
33	279	N I Y L L V P P V	15
34	285	P P V L N P I V Y	15
35	289	N P I V Y G V K T	15
36	9	S S A T Y F I L I	14
37	65	L C M L S G I D I	14
38	84	L A I F W F N S T	14
39	126	V A I C H P L R H	14
40	157	L M A P L P V F I	14
41	158	M A P L P V F I K	14
42	191	C D D I R V N V V	14
43	200	Y G L I V I I S A	14
44	209	I G L D S L L I S	14
45	215	L I S F S Y L L I	14
46	219	S Y L L I L K T V	14
47	220	Y L L I L K T V L	14
48	237	K A F G T C V S H	14
49	247	C A V F I F Y V P	14
50	249	V F I F Y V P F I	14
51	251	I F Y V P F I G L	14
52	257	I G L S M V H R F	14
53	268	R R D S P L P V I	14
54	273	L P V I L A N I Y	14
55	29	L A F P L C S L Y	13
56	33	L C S L Y L I A V	13
57	55	H S L H E P M Y I	13
58	67	M L S G I D I L I	13
59	80	M P K M L A I F W	13

HLA-B*5101 nonomers (SEQ ID
NOS 2064-2132, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
60	95	Q	F	D	A	C	L	L	Q	I	13
61	98	A	C	L	L	Q	I	F	A	I	13
62	104	F	A	I	H	S	L	S	G	M	13
63	146	I	G	V	A	A	V	V	R	G	13
64	148	V	A	A	V	V	R	G	A	A	13
65	153	R	G	A	A	L	M	A	P	L	13
66	233	E	A	Q	A	K	A	F	G	T	13
67	243	V	S	H	V	C	A	V	F	I	13
68	292	V	Y	G	V	K	T	K	E	I	13
69	296	K	T	K	E	I	R	Q	R	I	13

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Please replace Table XXVII, beginning at page 201, line 1, with the following rewritten

Table XXVII:

--Table XXVII:

HLA Class I decamers

HLA-A1 decamers (SEQ ID NOS
2133-2153, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	191	C	D	D	I	R	V	N	V	V	Y	27
2	244	S	H	V	C	A	V	F	I	F	Y	24
3	40	A	V	L	G	N	L	T	I	I	Y	21
4	284	V	P	P	V	L	N	P	I	V	Y	21
5	116	V	L	L	A	M	A	F	D	R	Y	20
6	28	W	L	A	F	P	L	C	S	L	Y	18
7	297	T	K	E	I	R	Q	R	I	L	R	17
8	21	G	L	E	E	A	Q	F	W	L	A	16
9	22	L	E	E	A	Q	F	W	L	A	F	16
10	52	R	T	E	H	S	L	H	E	P	M	16
11	53	T	E	H	S	L	H	E	P	M	Y	16
12	57	L	H	E	P	M	Y	I	F	L	C	16
13	111	G	M	E	S	T	V	L	L	A	M	16
14	272	P	L	P	V	I	L	A	N	I	Y	16
15	1	M	V	D	P	N	G	N	E	S	S	15
16	4	P	N	G	N	E	S	S	A	T	Y	15
17	121	A	F	D	R	Y	V	A	I	C	H	15
18	171	C	R	S	N	I	L	S	H	S	Y	15
19	211	L	D	S	L	L	I	S	F	S	Y	15
20	8	E	S	S	A	T	Y	F	I	L	I	13
21	190	A	C	D	D	I	R	V	N	V	V	13

HLA-A*0201 decamers (SEQ ID
NOS 2154-2253, respectively
in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	score
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HLA-A*0201 decamers (SEQ ID
NOS 2154-2253, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	221	L	L	I	L	K	<u>T</u>	V	L	G	L	30
2	100	L	L	Q	I	F	<u>A</u>	I	H	S	L	29
3	282	L	L	V	P	P	<u>V</u>	L	N	P	I	27
4	205	I	I	S	A	I	<u>G</u>	L	D	S	L	26
5	213	S	L	L	I	S	<u>F</u>	S	Y	L	L	25
6	56	S	L	H	E	P	<u>M</u>	Y	I	F	L	24
7	62	Y	I	F	L	C	<u>M</u>	L	S	G	I	24
8	108	S	L	S	G	M	<u>E</u>	S	T	V	L	24
9	117	L	L	A	M	A	<u>F</u>	D	R	Y	V	24
10	131	P	L	R	H	A	<u>T</u>	V	L	T	L	24
11	137	V	L	T	L	P	<u>R</u>	V	T	K	I	24
12	215	L	I	S	F	S	<u>Y</u>	L	L	I	L	24
13	38	L	I	A	V	L	<u>G</u>	N	L	T	I	23
14	41	V	L	G	N	L	<u>T</u>	I	I	Y	I	23
15	156	A	L	M	A	P	<u>L</u>	P	V	F	I	23
16	193	D	I	R	V	N	<u>V</u>	V	Y	G	L	23
17	214	L	L	I	S	F	<u>S</u>	Y	L	L	I	23
18	32	P	L	C	S	L	<u>Y</u>	L	I	A	V	22
19	119	A	M	A	F	D	<u>R</u>	Y	V	A	I	22
20	237	K	A	F	G	T	<u>C</u>	V	S	H	V	22
21	275	V	I	L	A	N	<u>I</u>	Y	L	L	V	22
22	85	A	I	F	W	F	<u>N</u>	S	T	T	I	21
23	139	T	L	P	R	V	<u>T</u>	K	I	G	V	21
24	202	L	I	V	I	I	<u>S</u>	A	I	G	L	21
25	13	Y	F	I	L	I	<u>G</u>	L	P	G	L	20
26	16	L	I	G	L	P	<u>G</u>	L	E	E	A	20
27	29	L	A	F	P	L	<u>C</u>	S	L	Y	L	20
28	142	R	V	T	K	I	<u>G</u>	V	A	A	V	20
29	148	V	A	A	V	V	<u>R</u>	G	A	A	L	20
30	167	Q	L	P	F	C	<u>R</u>	S	N	I	L	20
31	180	Y	C	L	H	Q	<u>D</u>	V	M	K	L	20
32	222	L	I	L	K	T	<u>V</u>	L	G	L	T	20
33	240	G	T	C	V	S	<u>H</u>	V	C	A	V	20
34	248	A	V	F	I	F	<u>Y</u>	V	P	F	I	20
35	250	F	I	F	Y	V	<u>P</u>	F	I	G	L	20
36	271	S	P	L	P	V	<u>I</u>	L	A	N	I	20
37	279	N	I	Y	L	L	<u>V</u>	P	P	V	L	20
38	304	I	L	R	L	F	<u>H</u>	V	A	T	H	20
39	10	S	A	T	Y	F	<u>I</u>	L	I	G	L	19
40	15	I	L	I	G	L	<u>P</u>	G	L	E	E	19
41	27	F	W	L	A	F	<u>P</u>	L	C	S	L	19
42	35	S	L	Y	L	I	<u>A</u>	V	L	G	N	19
43	37	Y	L	I	A	V	<u>L</u>	G	N	L	T	19
44	44	N	L	T	I	I	<u>Y</u>	I	V	R	T	19
45	64	F	L	C	M	L	<u>S</u>	G	I	D	I	19
46	83	M	L	A	I	F	<u>W</u>	F	N	S	T	19
47	159	A	P	L	P	V	<u>F</u>	I	K	Q	L	19
48	189	L	A	C	D	D	<u>I</u>	R	V	N	V	19
49	207	S	A	I	G	L	<u>D</u>	S	L	L	I	19
50	253	Y	V	P	F	I	<u>G</u>	L	S	M	V	19

HLA-A*0201 decamers (SEQ ID
NOS 2154-2253, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
51	276	I	L	A	N	I	<u>Y</u>	L	L	V	P	19
52	281	Y	L	L	V	P	<u>P</u>	V	L	N	P	19
53	283	L	V	P	P	V	<u>L</u>	N	P	I	V	19
54	286	P	V	L	N	P	<u>I</u>	V	Y	G	V	19
55	33	L	C	S	L	Y	<u>L</u>	I	A	V	L	18
56	36	L	Y	L	I	A	<u>V</u>	L	G	N	L	18
57	39	I	A	V	L	G	<u>N</u>	L	T	I	I	18
58	42	L	G	N	L	T	<u>I</u>	I	Y	I	V	18
59	66	C	M	L	S	G	<u>I</u>	D	I	L	I	18
60	111	G	M	E	S	T	<u>V</u>	L	L	A	M	18
61	128	I	C	H	P	L	<u>R</u>	H	A	T	V	18
62	134	H	A	T	V	L	<u>T</u>	L	P	R	V	18
63	154	G	A	A	L	M	<u>A</u>	P	L	P	V	18
64	157	L	M	A	P	L	<u>P</u>	V	F	I	K	18
65	190	A	C	D	D	I	<u>R</u>	V	N	V	V	18
66	229	G	L	T	R	E	<u>A</u>	Q	A	K	A	18
67	245	H	V	C	A	V	<u>F</u>	I	F	Y	V	18
68	274	P	V	I	L	A	<u>N</u>	I	Y	L	L	18
69	278	A	N	I	Y	L	<u>L</u>	V	P	P	V	18
70	291	I	V	Y	G	V	<u>K</u>	T	K	E	I	18
71	298	K	E	I	R	Q	<u>R</u>	I	L	R	L	18
72	48	I	Y	I	V	R	<u>T</u>	E	H	S	L	17
73	65	L	C	M	L	S	<u>G</u>	I	D	I	L	17
74	67	M	L	S	G	I	<u>D</u>	I	L	I	S	17
75	74	L	I	S	T	S	<u>S</u>	M	P	K	M	17
76	91	S	T	T	I	Q	<u>F</u>	D	A	C	L	17
77	94	I	Q	F	D	A	<u>C</u>	L	L	Q	I	17
78	188	K	L	A	C	D	<u>D</u>	I	R	V	N	17
79	197	N	V	V	Y	G	<u>L</u>	I	V	I	I	17
80	200	Y	G	L	I	V	<u>I</u>	I	S	A	I	17
81	218	F	S	Y	L	L	<u>I</u>	L	K	T	V	17
82	227	V	L	G	L	T	<u>R</u>	E	A	Q	A	17
83	303	R	I	L	R	L	<u>F</u>	H	V	A	T	17
84	21	G	L	E	E	A	<u>Q</u>	F	W	L	A	16
85	92	T	T	I	Q	F	<u>D</u>	A	C	L	L	16
86	97	D	A	C	L	L	<u>Q</u>	I	F	A	I	16
87	127	A	I	C	H	P	<u>L</u>	R	H	A	T	16
88	143	V	T	K	I	G	<u>V</u>	A	A	V	V	16
89	195	R	V	N	V	V	<u>Y</u>	G	L	I	V	16
90	220	Y	L	L	I	L	<u>K</u>	T	V	L	G	16
91	296	K	T	K	E	I	<u>R</u>	Q	R	I	L	16
92	18	G	L	P	G	L	<u>E</u>	E	A	Q	F	15
93	30	A	F	P	L	C	<u>S</u>	L	Y	L	I	15
94	126	V	A	I	C	H	<u>P</u>	L	R	H	A	15
95	145	K	I	G	V	A	<u>A</u>	V	V	R	G	15
96	173	S	N	I	L	S	<u>H</u>	S	Y	C	L	15
97	201	G	L	I	V	I	<u>I</u>	S	A	I	G	15
98	208	A	I	G	L	D	<u>S</u>	L	L	I	S	15
99	210	G	L	D	S	L	<u>L</u>	I	S	F	S	15
100	267	K	R	R	D	S	<u>P</u>	L	P	V	I	15

HLA-A*0201 decamers (SEQ ID
NOS 2154-2253, respectively
in order of appearance)

Pos 1 2 3 4 5 6 7 8 9 0 score

HLA-A*0203 decamers (SEQ ID
NOS 2254-2301, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	141	P	R	V	T	K	I	G	V	A	A	19
2	147	G	V	A	A	V	V	R	G	A	A	19
3	112	M	E	S	T	V	L	L	A	M	A	18
4	227	V	L	G	L	T	R	E	A	Q	A	18
5	229	G	L	T	R	E	A	Q	A	K	A	18
6	142	R	V	T	K	I	G	V	A	A	V	17
7	148	V	A	A	V	V	R	G	A	A	L	17
8	2	V	D	P	N	G	N	E	S	S	A	10
9	16	L	I	G	L	P	G	L	E	E	A	10
10	21	G	L	E	E	A	Q	F	W	L	A	10
11	31	F	P	L	C	S	L	Y	L	I	A	10
12	76	S	T	S	S	M	P	K	M	L	A	10
13	89	F	N	S	T	T	I	Q	F	D	A	10
14	96	F	D	A	C	L	L	Q	I	F	A	10
15	110	S	G	M	E	S	T	V	L	L	A	10
16	118	L	A	M	A	F	D	R	Y	V	A	10
17	126	V	A	I	C	H	P	L	R	H	A	10
18	140	L	P	R	V	T	K	I	G	V	A	10
19	146	I	G	V	A	A	V	V	R	G	A	10
20	150	A	V	V	R	G	A	A	L	M	A	10
21	181	C	L	H	Q	D	V	M	K	L	A	10
22	199	V	Y	G	L	I	V	I	I	S	A	10
23	225	K	T	V	L	G	L	T	R	E	A	10
24	239	F	G	T	C	V	S	H	V	C	A	10
25	269	R	D	S	P	L	P	V	I	L	A	10
26	302	Q	R	I	L	R	L	F	H	V	A	10
27	305	L	R	L	F	H	V	A	T	H	A	10
28	3	D	P	N	G	N	E	S	S	A	T	9
29	17	I	G	L	P	G	L	E	E	A	Q	9
30	22	L	E	E	A	Q	F	W	L	A	F	9
31	32	P	L	C	S	L	Y	L	I	A	V	9
32	77	T	S	S	M	P	K	M	L	A	I	9
33	90	N	S	T	T	I	Q	F	D	A	C	9
34	97	D	A	C	L	L	Q	I	F	A	I	9
35	111	G	M	E	S	T	V	L	L	A	M	9
36	113	E	S	T	V	L	L	A	M	A	F	9
37	119	A	M	A	F	D	R	Y	V	A	I	9
38	127	A	I	C	H	P	L	R	H	A	T	9
39	151	V	V	R	G	A	A	L	M	A	P	9
40	182	L	H	Q	D	V	M	K	L	A	C	9
41	200	Y	G	L	I	V	I	I	S	A	I	9
42	226	T	V	L	G	L	T	R	E	A	Q	9
43	228	L	G	L	T	R	E	A	Q	A	K	9

HLA-A*0203 decamers (SEQ ID
NOS 2254-2301, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
44	230	L	<u>T</u>	R	E	A	Q	<u>A</u>	K	A	F	9
45	240	G	<u>T</u>	C	V	S	H	<u>V</u>	C	A	V	9
46	270	D	<u>S</u>	P	L	P	V	<u>I</u>	L	A	N	9
47	303	R	<u>I</u>	L	R	L	F	<u>H</u>	V	A	T	9
48	306	R	<u>L</u>	F	H	V	A	<u>T</u>	H	A	S	9

HLA-A26 decamers (SEQ ID NOS
2302-2366, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	299	E	I	R	Q	R	I	L	R	L	F	31
2	193	D	I	R	V	N	V	V	Y	G	L	29
3	250	F	I	F	Y	V	P	F	I	G	L	25
4	256	F	I	G	L	S	M	V	H	R	F	25
5	74	L	I	S	T	S	S	M	P	K	M	24
6	274	P	V	I	L	A	N	I	Y	L	L	24
7	18	G	L	P	G	L	E	E	A	Q	F	23
8	116	V	L	L	A	M	A	F	D	R	Y	23
9	205	I	I	S	A	I	G	L	D	S	L	23
10	221	L	L	I	L	K	T	V	L	G	L	23
11	230	L	T	R	E	A	Q	A	K	A	F	23
12	13	Y	F	I	L	I	G	L	P	G	L	22
13	40	A	V	L	G	N	L	T	I	I	Y	22
14	56	S	L	H	E	P	M	Y	I	F	L	22
15	95	Q	F	D	A	C	L	L	Q	I	F	22
16	215	L	I	S	F	S	Y	L	L	I	L	22
17	92	T	T	I	Q	F	D	A	C	L	L	21
18	100	L	L	Q	I	F	A	I	H	S	L	21
19	103	I	F	A	I	H	S	L	S	G	M	21
20	296	K	T	K	E	I	R	Q	R	I	L	21
21	28	W	L	A	F	P	L	C	S	L	Y	20
22	131	P	L	R	H	A	T	V	L	T	L	20
23	59	E	P	M	Y	I	F	L	C	M	L	19
24	91	S	T	T	I	Q	F	D	A	C	L	19
25	202	L	I	V	I	I	S	A	I	G	L	19
26	212	D	S	L	L	I	S	F	S	Y	L	19
27	272	P	L	P	V	I	L	A	N	I	Y	19
28	279	N	I	Y	L	L	V	P	P	V	L	19
29	52	R	T	E	H	S	L	H	E	P	M	18
30	62	Y	I	F	L	C	M	L	S	G	I	18
31	72	D	I	L	I	S	T	S	S	M	P	18
32	108	S	L	S	G	M	E	S	T	V	L	18
33	113	E	S	T	V	L	L	A	M	A	F	18
34	151	V	V	R	G	A	A	L	M	A	P	18
35	78	S	S	M	P	K	M	L	A	I	F	17
36	142	R	V	T	K	I	G	V	A	A	V	17
37	162	P	V	F	I	K	Q	L	P	F	C	17
38	164	F	I	K	Q	L	P	F	C	R	S	17

HLA-A26 decamers (SEQ ID NOS
2302-2366, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
39	167	Q	L	P	F	C	R	S	N	I	L	17
40	185	D	V	M	K	L	A	C	D	D	I	17
41	248	A	V	F	I	F	Y	V	P	F	I	17
42	253	Y	V	P	F	I	G	L	S	M	V	17
43	45	L	T	I	I	Y	I	V	R	T	E	16
44	145	K	I	G	V	A	A	V	V	R	G	16
45	198	V	V	Y	G	L	I	V	I	I	S	16
46	203	I	V	I	I	S	A	I	G	L	D	16
47	209	I	G	L	D	S	L	L	I	S	F	16
48	213	S	L	L	I	S	F	S	Y	L	L	16
49	255	P	F	I	G	L	S	M	V	H	R	16
50	264	R	F	S	K	R	R	D	S	P	L	16
51	294	G	V	K	T	K	E	I	R	Q	R	16
52	16	L	I	G	L	P	G	L	E	E	A	15
53	80	M	P	K	M	L	A	I	F	W	F	15
54	114	S	T	V	L	L	A	M	A	F	D	15
55	155	A	A	L	M	A	P	L	P	V	F	15
56	159	A	P	L	P	V	F	I	K	Q	L	15
57	174	N	I	L	S	H	S	Y	C	L	H	15
58	197	N	V	V	Y	G	L	I	V	I	I	15
59	210	G	L	D	S	L	L	I	S	F	S	15
60	214	L	L	I	S	F	S	Y	L	L	I	15
61	222	L	I	L	K	T	V	L	G	L	T	15
62	240	G	T	C	V	S	H	V	C	A	V	15
63	247	C	A	V	F	I	F	Y	V	P	F	15
64	286	P	V	L	N	P	I	V	Y	G	V	15
65	298	K	E	I	R	Q	R	I	L	R	L	15

HLA-A3 decamers (SEQ ID NOS
2367-2432, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	136	T	V	<u>L</u>	T	L	<u>P</u>	<u>R</u>	V	T	K	31
2	287	V	L	<u>N</u>	P	I	<u>V</u>	<u>Y</u>	G	V	K	28
3	223	I	L	<u>K</u>	T	V	<u>L</u>	<u>G</u>	L	T	R	27
4	304	I	L	<u>R</u>	L	F	<u>H</u>	<u>V</u>	A	T	H	27
5	73	I	L	<u>I</u>	S	T	<u>S</u>	<u>S</u>	M	P	K	26
6	15	I	L	<u>I</u>	G	L	<u>P</u>	<u>G</u>	L	E	E	23
7	40	A	V	<u>L</u>	G	N	<u>L</u>	<u>T</u>	I	I	Y	23
8	150	A	V	<u>V</u>	R	G	<u>A</u>	<u>A</u>	L	M	A	23
9	258	G	L	<u>S</u>	M	V	<u>H</u>	<u>R</u>	F	S	K	23
10	18	G	L	<u>P</u>	G	L	<u>E</u>	<u>E</u>	A	Q	F	22
11	303	R	I	<u>L</u>	R	L	<u>F</u>	<u>H</u>	V	A	T	22
12	276	I	L	<u>A</u>	N	I	<u>Y</u>	<u>L</u>	L	V	P	21
13	28	W	L	<u>A</u>	F	P	<u>L</u>	<u>C</u>	S	L	Y	20
14	115	T	V	<u>L</u>	L	A	<u>M</u>	<u>A</u>	F	D	R	20
15	116	V	L	<u>L</u>	A	M	<u>A</u>	<u>F</u>	D	R	Y	20
16	125	Y	V	<u>A</u>	I	C	<u>H</u>	<u>P</u>	L	R	H	20
17	131	P	L	<u>R</u>	H	A	<u>T</u>	<u>V</u>	L	T	L	20
18	144	T	K	<u>I</u>	G	V	<u>A</u>	<u>A</u>	V	V	R	20

HLA-A3 decamers (SEQ ID NOS
2367-2432, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
19	156	A	L	<u>M</u>	A	P	<u>L</u>	P	V	F	I	20
20	195	R	V	<u>N</u>	V	V	<u>Y</u>	G	L	I	V	20
21	35	S	L	<u>Y</u>	L	I	<u>A</u>	V	L	G	N	19
22	272	P	L	<u>P</u>	V	I	<u>L</u>	A	N	I	Y	19
23	37	Y	L	<u>I</u>	A	V	<u>L</u>	G	N	L	T	18
24	49	Y	I	<u>V</u>	R	T	<u>E</u>	H	S	L	H	18
25	50	I	V	<u>R</u>	T	E	H	S	L	H	E	18
26	108	S	L	<u>S</u>	G	M	<u>E</u>	S	T	V	L	18
27	142	R	V	<u>T</u>	K	I	<u>G</u>	V	A	A	V	18
28	188	K	L	<u>A</u>	C	D	<u>D</u>	I	R	V	N	18
29	279	N	I	<u>Y</u>	L	L	<u>V</u>	P	P	V	L	18
30	291	I	V	<u>Y</u>	G	V	<u>K</u>	T	K	E	I	18
31	294	G	V	<u>K</u>	T	K	<u>E</u>	I	R	Q	R	18
32	46	T	I	<u>I</u>	Y	I	<u>V</u>	R	T	E	H	17
33	102	Q	I	<u>F</u>	A	I	<u>H</u>	S	L	S	G	17
34	151	V	V	<u>R</u>	G	A	<u>A</u>	L	M	A	P	17
35	179	S	Y	<u>C</u>	L	H	<u>Q</u>	D	V	M	K	17
36	203	I	V	<u>I</u>	I	S	<u>A</u>	I	G	L	D	17
37	204	V	I	<u>I</u>	S	A	<u>I</u>	G	L	D	S	17
38	220	Y	L	<u>L</u>	I	L	<u>K</u>	T	V	L	G	17
39	221	L	L	<u>I</u>	L	K	<u>T</u>	V	L	G	L	17
40	227	V	L	<u>G</u>	L	T	<u>R</u>	E	A	Q	A	17
41	242	C	V	<u>S</u>	H	V	<u>C</u>	A	V	F	I	17
42	289	N	P	<u>I</u>	V	Y	<u>G</u>	V	K	T	K	17
43	38	L	I	<u>A</u>	V	L	G	N	L	T	I	16
44	85	A	I	<u>F</u>	W	F	<u>N</u>	S	T	T	I	16
45	147	G	V	<u>A</u>	A	V	<u>V</u>	R	G	A	A	16
46	198	V	V	<u>Y</u>	G	L	<u>I</u>	V	I	I	S	16
47	201	G	L	<u>I</u>	V	I	<u>I</u>	S	A	I	G	16
48	214	L	L	<u>I</u>	S	F	<u>S</u>	Y	L	L	I	16
49	226	T	V	<u>L</u>	G	L	<u>T</u>	R	E	A	Q	16
50	228	L	G	<u>L</u>	T	R	<u>E</u>	A	Q	A	K	16
51	229	G	L	<u>T</u>	R	E	<u>A</u>	Q	A	K	A	16
52	1	M	V	<u>D</u>	P	N	<u>G</u>	N	E	S	S	15
53	44	N	L	<u>T</u>	I	I	<u>Y</u>	I	V	R	T	15
54	47	I	I	<u>Y</u>	I	V	<u>R</u>	T	E	H	S	15
55	67	M	L	<u>S</u>	G	I	<u>D</u>	I	L	I	S	15
56	72	D	I	<u>L</u>	I	S	<u>T</u>	S	S	M	P	15
57	99	C	L	<u>L</u>	Q	I	<u>F</u>	A	I	H	S	15
58	105	A	I	<u>H</u>	S	L	<u>S</u>	G	M	E	S	15
59	145	K	I	<u>G</u>	V	A	<u>A</u>	V	V	R	G	15
60	175	I	L	<u>S</u>	H	S	<u>Y</u>	C	L	H	Q	15
61	191	C	D	<u>D</u>	I	R	<u>V</u>	N	V	V	Y	15
62	208	A	I	<u>G</u>	L	D	<u>S</u>	L	L	I	S	15
63	275	V	I	<u>L</u>	A	N	<u>I</u>	Y	L	L	V	15
64	281	Y	L	<u>L</u>	V	P	<u>P</u>	V	L	N	P	15
65	299	E	I	<u>R</u>	Q	R	<u>I</u>	L	R	L	F	15
66	306	R	L	<u>F</u>	H	V	<u>A</u>	T	H	A	S	15

HLA-B*0702 decamers (SEQ ID

NOS 2433-2492, respectively
in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	score	
1	159	A	P	L	P	V	F	I	K	Q	L	23
2	59	E	P	M	Y	I	F	L	C	M	L	22
3	273	L	P	V	I	L	A	N	I	Y	L	20
4	3	D	P	N	G	N	E	S	S	A	T	19
5	130	H	P	L	R	H	A	T	V	L	T	19
6	140	L	P	R	V	T	K	I	G	V	A	19
7	161	L	P	V	F	I	K	Q	L	P	F	19
8	31	F	P	L	C	S	L	Y	L	I	A	18
9	271	S	P	L	P	V	I	L	A	N	I	18
10	80	M	P	K	M	L	A	I	F	W	F	16
11	108	S	L	S	G	M	E	S	T	V	L	16
12	131	P	L	R	H	A	T	V	L	T	L	15
13	264	R	F	S	K	R	R	D	S	P	L	15
14	33	L	C	S	L	Y	L	I	A	V	L	14
15	109	L	S	G	M	E	S	T	V	L	L	14
16	152	V	R	G	A	A	L	M	A	P	L	14
17	205	I	I	S	A	I	G	L	D	S	L	14
18	215	L	I	S	F	S	Y	L	L	I	L	14
19	268	R	R	D	S	P	L	P	V	I	L	14
20	29	L	A	F	P	L	C	S	L	Y	L	13
21	148	V	A	A	V	V	R	G	A	A	L	13
22	156	A	L	M	A	P	L	P	V	F	I	13
23	193	D	I	R	V	N	V	V	Y	G	L	13
24	221	L	L	I	L	K	T	V	L	G	L	13
25	298	K	E	I	R	Q	R	I	L	R	L	13
26	7	N	E	S	S	A	T	Y	F	I	L	12
27	19	L	P	G	L	E	E	A	Q	F	W	12
28	24	E	A	Q	F	W	L	A	F	P	L	12
29	119	A	M	A	F	D	R	Y	V	A	I	12
30	129	C	H	P	L	R	H	A	T	V	L	12
31	206	I	S	A	I	G	L	D	S	L	L	12
32	219	S	Y	L	L	I	L	K	T	V	L	12
33	279	N	I	Y	L	L	V	P	P	V	L	12
34	285	P	P	V	L	N	P	I	V	Y	G	12
35	8	E	S	S	A	T	Y	F	I	L	I	11
36	13	Y	F	I	L	I	G	L	P	G	L	11
37	27	F	W	L	A	F	P	L	C	S	L	11
38	48	I	Y	I	V	R	T	E	H	S	L	11
39	56	S	L	H	E	P	M	Y	I	F	L	11
40	65	L	C	M	L	S	G	I	D	I	L	11
41	75	I	S	T	S	S	M	P	K	M	L	11
42	77	T	S	S	M	P	K	M	L	A	I	11
43	91	S	T	T	I	Q	F	D	A	C	L	11
44	123	D	R	Y	V	A	I	C	H	P	L	11
45	142	R	V	T	K	I	G	V	A	A	V	11
46	180	Y	C	L	H	Q	D	V	M	K	L	11
47	190	A	C	D	D	I	R	V	N	V	V	11
48	212	D	S	L	L	I	S	F	S	Y	L	11
49	234	A	Q	A	K	A	F	G	T	C	V	11
50	242	C	V	S	H	V	C	A	V	F	I	11
51	248	A	V	F	I	F	Y	V	P	F	I	11

HLA-B*0702 decamers (SEQ ID
NOS 2433-2492, respectively
in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	score
52 250	F	I	F	Y	V	P	F	I	G	L	11
53 254	V	P	F	I	G	L	S	M	V	H	11
54 266	S	K	R	R	D	S	P	L	P	V	11
55 267	K	R	R	D	S	P	L	P	V	I	11
56 269	R	D	S	P	L	P	V	I	L	A	11
57 278	A	N	I	Y	L	L	V	P	P	V	11
58 284	V	P	P	V	L	N	P	I	V	Y	11
59 289	N	P	I	V	Y	G	V	K	T	K	11
60 296	K	T	K	E	I	R	Q	R	I	L	11

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Please replace Table XXVIII, beginning at page 205, line 1, with the following rewritten

Table XXVIII:

--Table XXVIII:

HLA Class II Epitopes (sample 15-mer length)

(SEQ ID NOS 2493-2595, respectively in order of appearance)

HLA-DRB1*0101 15-mers

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1 200	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	L	36
2 68	L	S	G	I	D	I	L	I	S	T	S	S	M	P	K	34
3 62	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	S	33
4 103	I	F	A	I	H	S	L	S	G	M	E	S	T	V	L	32
5 45	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	31
6 193	D	I	R	V	N	V	V	Y	G	L	I	V	I	I	S	31
7 277	L	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	31
8 97	D	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	30
9 106	I	H	S	L	S	G	M	E	S	T	V	L	L	A	M	30
10 240	G	T	C	V	S	H	V	C	A	V	F	I	F	Y	V	30
11 10	S	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	29
12 289	N	P	I	V	Y	G	V	K	T	K	E	I	R	Q	R	29
13 11	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	28
14 250	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	R	27
15 140	L	P	R	V	T	K	I	G	V	A	A	V	V	R	G	26
16 183	H	Q	D	V	M	K	L	A	C	D	D	I	R	V	N	26
17 217	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	26
18 16	L	I	G	L	P	G	L	E	E	A	Q	F	W	L	A	25
19 24	E	A	Q	F	W	L	A	F	P	L	C	S	L	Y	L	25
20 36	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	I	25
21 70	G	I	D	I	L	I	S	T	S	S	M	P	K	M	L	25
22 111	G	M	E	S	T	V	L	L	A	M	A	F	D	R	Y	25
23 148	V	A	A	V	V	R	G	A	A	L	M	A	P	L	P	25
24 162	P	V	F	I	K	Q	L	P	F	C	R	S	N	I	L	25
25 197	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	L	25
26 211	L	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	25

HLA-DRB1*0101 15-mers

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
27 218	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	25
28 13	Y	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	24
29 30	A	F	P	L	C	S	L	Y	L	I	A	V	L	G	N	24
30 39	I	A	V	L	G	N	L	T	I	I	Y	I	V	R	T	24
31 77	T	S	S	M	P	K	M	L	A	I	F	W	F	N	S	24
32 85	A	I	F	W	F	N	S	T	T	I	Q	F	D	A	C	24
33 137	V	L	T	L	P	R	V	T	K	I	G	V	A	A	V	24
34 151	V	V	R	G	A	A	L	M	A	P	L	P	V	F	I	24
35 161	L	P	V	F	I	K	Q	L	P	F	C	R	S	N	I	24
36 196	V	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	24
37 202	L	I	V	I	I	S	A	I	G	L	D	S	L	L	I	24
38 208	A	I	G	L	D	S	L	L	I	S	F	S	Y	L	L	24
39 248	A	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	24
40 251	I	F	Y	V	P	F	I	G	L	S	M	V	H	R	F	24
41 83	M	L	A	I	F	W	F	N	S	T	T	I	Q	F	D	23
42 101	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	T	23
43 165	I	K	Q	L	P	F	C	R	S	N	I	L	S	H	S	23
44 203	I	V	I	I	S	A	I	G	L	D	S	L	L	I	S	23
45 221	L	L	I	L	K	T	V	L	G	L	T	R	E	A	Q	23
46 278	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	V	23
47 27	F	W	L	A	F	P	L	C	S	L	Y	L	I	A	V	22
48 35	S	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	22
49 61	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	22
50 65	L	C	M	L	S	G	I	D	I	L	I	S	T	S	S	22
51 80	M	P	K	M	L	A	I	F	W	F	N	S	T	T	I	22
52 145	K	I	G	V	A	A	V	V	R	G	A	A	L	M	A	22
53 146	I	G	V	A	A	V	V	R	G	A	A	L	M	A	P	22
54 154	G	A	A	L	M	A	P	L	P	V	F	I	K	Q	L	22
55 205	I	I	S	A	I	G	L	D	S	L	L	I	S	F	S	22
56 243	V	S	H	V	C	A	V	F	I	F	Y	V	P	F	I	22
57 270	D	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	22
58 274	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	L	22
59 281	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	V	22
60 34	C	S	L	Y	L	I	A	V	L	G	N	L	T	I	I	21
61 69	S	G	I	D	I	L	I	S	T	S	S	M	P	K	M	21
62 152	V	R	G	A	A	L	M	A	P	L	P	V	F	I	K	21
63 299	E	I	R	Q	R	I	L	R	L	F	H	V	A	T	H	21
64 100	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	20
65 135	A	T	V	L	T	L	P	R	V	T	K	I	G	V	A	20
66 141	P	R	V	T	K	I	G	V	A	A	V	V	R	G	A	20
67 191	C	D	D	I	R	V	N	V	V	Y	G	L	I	V	I	20
68 199	V	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	20
69 262	V	H	R	F	S	K	R	R	D	S	P	L	P	V	I	20
70 271	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	20
71 28	W	L	A	F	P	L	C	S	L	Y	L	I	A	V	L	19
72 58	H	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	19
73 59	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	19
74 60	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	19
75 98	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	19
76 215	L	I	S	F	S	Y	L	L	I	L	K	T	V	L	G	19
77 219	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	E	19

HLA-DRB1*0101 15-mers

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
78 228	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	C	19
79 232	R	E	A	Q	A	K	A	F	G	T	C	V	S	H	V	19
80 246	V	C	A	V	F	I	F	Y	V	P	F	I	G	L	S	19
81 297	T	K	E	I	R	Q	R	I	L	R	L	F	H	V	A	19
82 3	D	P	N	G	N	E	S	S	A	T	Y	F	I	L	I	18
83 14	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	W	18
84 25	A	Q	F	W	L	A	F	P	L	C	S	L	Y	L	I	18
85 42	L	G	N	L	T	I	I	Y	I	V	R	T	E	H	S	18
86 46	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	18
87 78	S	S	M	P	K	M	L	A	I	F	W	F	N	S	T	18
88 84	L	A	I	F	W	F	N	S	T	T	I	Q	F	D	A	18
89 89	F	N	S	T	T	I	Q	F	D	A	C	L	L	Q	I	18
90 93	T	I	Q	F	D	A	C	L	L	Q	I	F	A	I	H	18
91 115	T	V	L	L	A	M	A	F	D	R	Y	V	A	I	C	18
92 119	A	M	A	F	D	R	Y	V	A	I	C	H	P	L	R	18
93 127	A	I	C	H	P	L	R	H	A	T	V	L	T	L	P	18
94 129	C	H	P	L	R	H	A	T	V	L	T	L	P	R	V	18
95 147	G	V	A	A	V	V	R	G	A	A	L	M	A	P	L	18
96 149	A	A	V	V	R	G	A	A	L	M	A	P	L	P	V	18
97 216	I	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	18
98 227	V	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	18
99 249	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	18
100 253	Y	V	P	F	I	G	L	S	M	V	H	R	F	S	K	18
101 284	V	P	P	V	L	N	P	I	V	Y	G	V	K	T	K	18
102 286	P	V	L	N	P	I	V	Y	G	V	K	T	K	E	I	18
103 303	R	I	L	R	L	F	H	V	A	T	H	A	S	E	P	18

HLA-DRB1*0301 (DR17) 15-mers

(SEQ ID NOS 2596-2671, respectively in
order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1 16	L	I	G	L	P	G	L	E	E	A	Q	F	W	L	A	26
2 206	I	S	A	I	G	L	D	S	L	L	I	S	F	S	Y	23
3 91	S	T	T	I	Q	F	D	A	C	L	L	Q	I	F	A	22
4 117	L	L	A	M	A	F	D	R	Y	V	A	I	C	H	P	22
5 38	L	I	A	V	L	G	N	L	T	I	I	Y	I	V	R	21
6 179	S	Y	C	L	H	Q	D	V	M	K	L	A	C	D	D	21
7 211	L	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	21
8 219	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	E	21
9 272	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	P	21
10 26	Q	F	W	L	A	F	P	L	C	S	L	Y	L	I	A	20
11 114	S	T	V	L	L	A	M	A	F	D	R	Y	V	A	I	20
12 129	C	H	P	L	R	H	A	T	V	L	T	L	P	R	V	20
13 134	H	A	T	V	L	T	L	P	R	V	T	K	I	G	V	20
14 186	V	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	20
15 200	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	L	20
16 270	D	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	20
17 297	T	K	E	I	R	Q	R	I	L	R	L	F	H	V	A	20
18 11	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	19
19 54	E	H	S	L	H	E	P	M	Y	I	F	L	C	M	L	19

HLA-DRB1*0301 (DR17) 15-mers
(SEQ ID NOS 2596-2671, respectively in
order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
20 106	I	H	S	L	S	G	M	E	S	T	V	L	L	A	M	19
21 165	I	K	Q	L	P	F	C	R	S	N	I	L	S	H	S	19
22 191	C	D	D	I	R	V	N	V	V	Y	G	L	I	V	I	19
23 203	I	V	I	I	S	A	I	G	L	D	S	L	L	I	S	19
24 213	S	L	L	I	S	F	S	Y	L	L	I	L	K	T	V	19
25 224	L	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	19
26 227	V	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	19
27 248	A	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	19
28 254	V	P	F	I	G	L	S	M	V	H	R	F	S	K	R	19
29 277	L	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	19
30 36	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	I	18
31 93	T	I	Q	F	D	A	C	L	L	Q	I	F	A	I	H	18
32 98	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	18
33 125	Y	V	A	I	C	H	P	L	R	H	A	T	V	L	T	18
34 158	M	A	P	L	P	V	F	I	K	Q	L	P	F	C	R	18
35 187	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	G	18
36 217	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	18
37 225	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	F	18
38 281	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	V	18
39 288	L	N	P	I	V	Y	G	V	K	T	K	E	I	R	Q	18
40 18	G	L	P	G	L	E	E	A	Q	F	W	L	A	F	P	17
41 44	N	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	17
42 145	K	I	G	V	A	A	V	V	R	G	A	A	L	M	A	17
43 159	A	P	L	P	V	F	I	K	Q	L	P	F	C	R	S	17
44 256	F	I	G	L	S	M	V	H	R	F	S	K	R	R	D	17
45 259	L	S	M	V	H	R	F	S	K	R	R	D	S	P	L	17
46 137	V	L	T	L	P	R	V	T	K	I	G	V	A	A	V	16
47 262	V	H	R	F	S	K	R	R	D	S	P	L	P	V	I	16
48 294	G	V	K	T	K	E	I	R	Q	R	I	L	R	L	F	16
49 46	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	15
50 51	V	R	T	E	H	S	L	H	E	P	M	Y	I	F	L	15
51 172	R	S	N	I	L	S	H	S	Y	C	L	H	Q	D	V	15
52 189	L	A	C	D	D	I	R	V	N	V	V	Y	G	L	I	15
53 212	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	T	15
54 218	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	15
55 271	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	15
56 279	N	I	Y	L	L	V	P	P	V	L	N	P	I	V	Y	15
57 12	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	Q	14
58 35	S	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	14
59 64	F	L	C	M	L	S	G	I	D	I	L	I	S	T	S	14
60 140	L	P	R	V	T	K	I	G	V	A	A	V	V	R	G	14
61 273	L	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	14
62 301	R	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	14
63 13	Y	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	13
64 47	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	M	13
65 71	I	D	I	L	I	S	T	S	S	M	P	K	M	L	A	13
66 80	M	P	K	M	L	A	I	F	W	F	N	S	T	T	I	13
67 109	L	S	G	M	E	S	T	V	L	L	A	M	A	F	D	13
68 113	E	S	T	V	L	L	A	M	A	F	D	R	Y	V	A	13

HLA-DRB1*0301 (DR17) 15-mers
(SEQ ID NOS 2596-2671, respectively in
order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
69 135	A	T	V	L	T	L	P	R	V	T	K	I	G	V	A	13
70 195	R	V	N	V	V	Y	G	L	I	V	I	I	S	A	I	13
71 202	L	I	V	I	I	S	A	I	G	L	D	S	L	L	I	13
72 220	Y	L	L	I	L	K	T	V	L	G	L	T	R	E	A	13
73 221	L	L	I	L	K	T	V	L	G	L	T	R	E	A	Q	13
74 264	R	F	S	K	R	R	D	S	P	L	P	V	I	L	A	13
75 280	I	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	13
76 302	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	E	13

HLA-DRB1*0401 (DR4Dw4) 15-mers
(SEQ ID NOS 2672-2805, respectively in
order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1 36	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	I	26
2 45	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	26
3 68	L	S	G	I	D	I	L	I	S	T	S	S	M	P	K	26
4 83	M	L	A	I	F	W	F	N	S	T	T	I	Q	F	D	26
5 134	H	A	T	V	L	T	L	P	R	V	T	K	I	G	V	26
6 145	K	I	G	V	A	A	V	V	R	G	A	A	L	M	A	26
7 224	L	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	26
8 227	V	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	26
9 256	F	I	G	L	S	M	V	H	R	F	S	K	R	R	D	26
10 281	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	V	26
11 289	N	P	I	V	Y	G	V	K	T	K	E	I	R	Q	R	26
12 301	R	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	26
13 11	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	22
14 24	E	A	Q	F	W	L	A	F	P	L	C	S	L	Y	L	22
15 25	A	Q	F	W	L	A	F	P	L	C	S	L	Y	L	I	22
16 34	C	S	L	Y	L	I	A	V	L	G	N	L	T	I	I	22
17 84	L	A	I	F	W	F	N	S	T	T	I	Q	F	D	A	22
18 122	F	D	R	Y	V	A	I	C	H	P	L	R	H	A	T	22
19 197	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	L	22
20 215	L	I	S	F	S	Y	L	L	I	L	K	T	V	L	G	22
21 217	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	22
22 250	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	R	22
23 278	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	V	22
24 19	L	P	G	L	E	E	A	Q	F	W	L	A	F	P	L	20
25 30	A	F	P	L	C	S	L	Y	L	I	A	V	L	G	N	20
26 33	L	C	S	L	Y	L	I	A	V	L	G	N	L	T	I	20
27 35	S	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	20
28 39	I	A	V	L	G	N	L	T	I	I	Y	I	V	R	T	20
29 42	L	G	N	L	T	I	I	Y	I	V	R	T	E	H	S	20
30 44	N	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	20
31 48	I	Y	I	V	R	T	E	H	S	L	H	E	P	M	Y	20
32 58	H	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	20
33 62	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	S	20
34 65	L	C	M	L	S	G	I	D	I	L	I	S	T	S	S	20
35 71	I	D	I	L	I	S	T	S	S	M	P	K	M	L	A	20

HLA-DRB1*0401 (DR4Dw4) 15-mers
(SEQ ID NOS 2672-2805, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
36	80	M	P	K	M	L	A	I	F	W	F	N	S	T	T	I	20
37	81	P	K	M	L	A	I	F	W	F	N	S	T	T	I	Q	20
38	91	S	T	T	I	Q	F	D	A	C	L	L	Q	I	F	A	20
39	97	D	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	20
40	98	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	20
41	100	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	20
42	103	I	F	A	I	H	S	L	S	G	M	E	S	T	V	L	20
43	106	I	H	S	L	S	G	M	E	S	T	V	L	L	A	M	20
44	115	T	V	L	L	A	M	A	F	D	R	Y	V	A	I	C	20
45	117	L	L	A	M	A	F	D	R	Y	V	A	I	C	H	P	20
46	125	Y	V	A	I	C	H	P	L	R	H	A	T	V	L	T	20
47	129	C	H	P	L	R	H	A	T	V	L	T	L	P	R	V	20
48	137	V	L	T	L	P	R	V	T	K	I	G	V	A	A	V	20
49	140	L	P	R	V	T	K	I	G	V	A	A	V	V	R	G	20
50	155	A	A	L	M	A	P	L	P	V	F	I	K	Q	L	P	20
51	162	P	V	F	I	K	Q	L	P	F	C	R	S	N	I	L	20
52	165	I	K	Q	L	P	F	C	R	S	N	I	L	S	H	S	20
53	179	S	Y	C	L	H	Q	D	V	M	K	L	A	C	D	D	20
54	183	H	Q	D	V	M	K	L	A	C	D	D	I	R	V	N	20
55	186	V	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	20
56	193	D	I	R	V	N	V	V	Y	G	L	I	V	I	I	S	20
57	196	V	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	20
58	199	V	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	20
59	200	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	L	20
60	202	L	I	V	I	I	S	A	I	G	L	D	S	L	L	I	20
61	203	I	V	I	I	S	A	I	G	L	D	S	L	L	I	S	20
62	206	I	S	A	I	G	L	D	S	L	L	I	S	F	S	Y	20
63	208	A	I	G	L	D	S	L	L	I	S	F	S	Y	L	L	20
64	211	L	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	20
65	212	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	T	20
66	218	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	20
67	240	G	T	C	V	S	H	V	C	A	V	F	I	F	Y	V	20
68	243	V	S	H	V	C	A	V	F	I	F	Y	V	P	F	I	20
69	246	V	C	A	V	F	I	F	Y	V	P	F	I	G	L	S	20
70	248	A	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	20
71	251	I	F	Y	V	P	F	I	G	L	S	M	V	H	R	F	20
72	272	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	P	20
73	277	L	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	20
74	285	P	P	V	L	N	P	I	V	Y	G	V	K	T	K	E	20
75	18	G	L	P	G	L	E	E	A	Q	F	W	L	A	F	P	18
76	27	F	W	L	A	F	P	L	C	S	L	Y	L	I	A	V	18
77	69	S	G	I	D	I	L	I	S	T	S	S	M	P	K	M	18
78	94	I	Q	F	D	A	C	L	L	Q	I	F	A	I	H	S	18
79	99	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	18
80	107	H	S	L	S	G	M	E	S	T	V	L	L	A	M	A	18
81	116	V	L	L	A	M	A	F	D	R	Y	V	A	I	C	H	18
82	126	V	A	I	C	H	P	L	R	H	A	T	V	L	T	L	18
83	164	F	I	K	Q	L	P	F	C	R	S	N	I	L	S	H	18
84	176	L	S	H	S	Y	C	L	H	Q	D	V	M	K	L	A	18

HLA-DRB1*0401 (DR4Dw4) 15-mers
(SEQ ID NOS 2672-2805, respectively in
order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
85	187	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	G	18
86	205	I	I	S	A	I	G	L	D	S	L	L	I	S	F	S	18
87	233	E	A	Q	A	K	A	F	G	T	C	V	S	H	V	C	18
88	237	K	A	F	G	T	C	V	S	H	V	C	A	V	F	I	18
89	271	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	18
90	293	Y	G	V	K	T	K	E	I	R	Q	R	I	L	R	L	18
91	294	G	V	K	T	K	E	I	R	Q	R	I	L	R	L	F	18
92	10	S	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	16
93	28	W	L	A	F	P	L	C	S	L	Y	L	I	A	V	L	16
94	59	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	16
95	61	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	16
96	85	A	I	F	W	F	N	S	T	T	I	Q	F	D	A	C	16
97	101	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	T	16
98	177	S	H	S	Y	C	L	H	Q	D	V	M	K	L	A	C	16
99	236	A	K	A	F	G	T	C	V	S	H	V	C	A	V	F	16
100	249	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	16
101	253	Y	V	P	F	I	G	L	S	M	V	H	R	F	S	K	16
102	13	Y	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	14
103	14	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	W	14
104	16	L	I	G	L	P	G	L	E	E	A	Q	F	W	L	A	14
105	38	L	I	A	V	L	G	N	L	T	I	I	Y	I	V	R	14
106	47	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	M	14
107	54	E	H	S	L	H	E	P	M	Y	I	F	L	C	M	L	14
108	60	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	14
109	64	F	L	C	M	L	S	G	I	D	I	L	I	S	T	S	14
110	70	G	I	D	I	L	I	S	T	S	S	M	P	K	M	L	14
111	72	D	I	L	I	S	T	S	S	M	P	K	M	L	A	I	14
112	109	L	S	G	M	E	S	T	V	L	L	A	M	A	F	D	14
113	113	E	S	T	V	L	L	A	M	A	F	D	R	Y	V	A	14
114	135	A	T	V	L	T	L	P	R	V	T	K	I	G	V	A	14
115	143	V	T	K	I	G	V	A	A	V	V	R	G	A	A	L	14
116	148	V	A	A	V	V	R	G	A	A	L	M	A	P	L	P	14
117	149	A	A	V	V	R	G	A	A	L	M	A	P	L	P	V	14
118	154	G	A	A	L	M	A	P	L	P	V	F	I	K	Q	L	14
119	158	M	A	P	L	P	V	F	I	K	Q	L	P	F	C	R	14
120	173	S	N	I	L	S	H	S	Y	C	L	H	Q	D	V	M	14
121	184	Q	D	V	M	K	L	A	C	D	D	I	R	V	N	V	14
122	191	C	D	D	I	R	V	N	V	V	Y	G	L	I	V	I	14
123	195	R	V	N	V	V	Y	G	L	I	V	I	I	S	A	I	14
124	213	S	L	L	I	S	F	S	Y	L	L	I	L	K	T	V	14
125	220	Y	L	L	I	L	K	T	V	L	G	L	T	R	E	A	14
126	221	L	L	I	L	K	T	V	L	G	L	T	R	E	A	Q	14
127	225	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	F	14
128	259	L	S	M	V	H	R	F	S	K	R	R	D	S	P	L	14
129	270	D	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	14
130	273	L	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	14
131	274	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	L	14
132	280	I	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	14
133	284	V	P	P	V	L	N	P	I	V	Y	G	V	K	T	K	14

HLA-DRB1*0401 (DR4Dw4) 15-mers
(SEQ ID NOS 2672-2805, respectively in
order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
134 302	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	E	14

HLA-DRB1*1101 15-mers
(SEQ ID NOS 2806-2866, respectively
in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1 145	K	I	G	V	A	A	V	V	R	G	A	A	L	M	A	28
2 122	F	D	R	Y	V	A	I	C	H	P	L	R	H	A	T	25
3 217	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	25
4 197	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	L	24
5 10	S	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	23
6 255	P	F	I	G	L	S	M	V	H	R	F	S	K	R	R	23
7 44	N	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	22
8 59	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	22
9 158	M	A	P	L	P	V	F	I	K	Q	L	P	F	C	R	22
10 237	K	A	F	G	T	C	V	S	H	V	C	A	V	F	I	22
11 74	L	I	S	T	S	S	M	P	K	M	L	A	I	F	W	21
12 134	H	A	T	V	L	T	L	P	R	V	T	K	I	G	V	20
13 137	V	L	T	L	P	R	V	T	K	I	G	V	A	A	V	20
14 162	P	V	F	I	K	Q	L	P	F	C	R	S	N	I	L	20
15 199	V	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	20
16 224	L	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	20
17 256	F	I	G	L	S	M	V	H	R	F	S	K	R	R	D	20
18 290	P	I	V	Y	G	V	K	T	K	E	I	R	Q	R	I	20
19 301	R	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	20
20 65	L	C	M	L	S	G	I	D	I	L	I	S	T	S	S	19
21 100	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	19
22 196	V	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	19
23 218	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	19
24 247	C	A	V	F	I	F	Y	V	P	F	I	G	L	S	M	19
25 274	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	L	19
26 45	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	18
27 68	L	S	G	I	D	I	L	I	S	T	S	S	M	P	K	18
28 80	M	P	K	M	L	A	I	F	W	F	N	S	T	T	I	18
29 97	D	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	18
30 103	I	F	A	I	H	S	L	S	G	M	E	S	T	V	L	18
31 208	A	I	G	L	D	S	L	L	I	S	F	S	Y	L	L	18
32 249	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	18
33 61	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	17
34 215	L	I	S	F	S	Y	L	L	I	L	K	T	V	L	G	17
35 259	L	S	M	V	H	R	F	S	K	R	R	D	S	P	L	17
36 278	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	V	17
37 288	L	N	P	I	V	Y	G	V	K	T	K	E	I	R	Q	17
38 11	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	16
39 24	E	A	Q	F	W	L	A	F	P	L	C	S	L	Y	L	16
40 42	L	G	N	L	T	I	I	Y	I	V	R	T	E	H	S	16
41 253	Y	V	P	F	I	G	L	S	M	V	H	R	F	S	K	16
42 47	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	M	15

HLA-DRB1*1101 15-mers
(SEQ ID NOS 2806-2866, respectively
in order of appearance)

Pos		1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
43	99	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	15
44	116	V	L	L	A	M	A	F	D	R	Y	V	A	I	C	H	15
45	143	V	T	K	I	G	V	A	A	V	V	R	G	A	A	L	15
46	179	S	Y	C	L	H	Q	D	V	M	K	L	A	C	D	D	15
47	227	V	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	15
48	260	S	M	V	H	R	F	S	K	R	R	D	S	P	L	P	15
49	261	M	V	H	R	F	S	K	R	R	D	S	P	L	P	V	15
50	277	L	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	15
51	285	P	P	V	L	N	P	I	V	Y	G	V	K	T	K	E	15
52	114	S	T	V	L	L	A	M	A	F	D	R	Y	V	A	I	14
53	125	Y	V	A	I	C	H	P	L	R	H	A	T	V	L	T	14
54	126	V	A	I	C	H	P	L	R	H	A	T	V	L	T	L	14
55	140	L	P	R	V	T	K	I	G	V	A	A	V	V	R	G	14
56	170	F	C	R	S	N	I	L	S	H	S	Y	C	L	H	Q	14
57	180	Y	C	L	H	Q	D	V	M	K	L	A	C	D	D	I	14
58	193	D	I	R	V	N	V	V	Y	G	L	I	V	I	I	S	14
59	229	G	L	T	R	E	A	Q	A	K	A	F	G	T	C	V	14
60	270	D	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	14
61	298	K	E	I	R	O	R	I	L	R	L	F	H	V	A	T	14

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Please replace Table XXIX, beginning at page 213, line 1, with the following rewritten
Table XXIX:

--Table XXIX. Nucleotide sequence in the 5' region close to 101P3A11 gene (SEQ ID NO:
2867).

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1 TGCCTCCAC CAAGCCTGGC TAACTTTTGC ATTTTAAATA GAGGCAGGGT TTCACCATGT
61 TGGCCTGGCT GGTCTCGAAC CCCTGACCTT GCGATCTGCC CACCTCGGCC TCCCAAAGTG
121 CTGGGATTAC AGGCGTGAGC CACTGTACCT GCGGGGCTT ATTGTTTTTT AAAAAGATTT
181 CAAAACCTT GCCCTGGCAA TTCTGATTTT CTGGGCCTGG AGCAGGACCT GGAGGGATGG
241 TGTTGTCAAT TACTTTAGAT GTTTCTATCA GGAAAGTTTG AGAAATGGTA TTCAGGCCTA
301 AACACAAACC TCTCTTGAAG TCTCATCCCA GACTGAGCCC CTGCTCCCTA TCTTAAATTA
361 GATTATAGTA GGTCTTAAAG TCAGCTGTAG ACTGAGCCTC TAAATCTGAA CCCAGACCCA
421 CCCTAACCCC AGGATACATC AGAAGAGCTG GTCAATGTGG ACCATTCTGA GCAATCCTGC
481 AAGTCTACTC TGATGGGAAA AGGCTAAGAG CAGTGCCCTG GGCAGCAACA TCAGCTCTGA
541 AGATGCAGGA CTGTGTTACA TGTTTTATGA GTGGGTCTTC ACACACTGAG ATTCATGGGA
601 CAGTAATAGA ATCTGCTTGT GCAGCACTGG GGCCTTGGAG GGTCAGGGTA AGGCTCAAGA
661 TGTCCAGGAA GTTGTATATA AGGAGAATCA GAGCAGAGAG AGACTAGGGT TCAGAATTAC
721 CAGGATGACT TAGTCCTGTT TGTTACTGTC ACCACTCCAA TGCCTTTTCC TCATTAGTCC
781 TTTCTCTCCT CTGAGCCACA ACTAAATGAT GTTTCTACTT TTCCCTTTCT ACTTTCCTAG
841 ACCCTGGATT TTGTATGCAG AAGCCCCAGC TCTTGGTCCC TATCATAGCC ACTTCAAATG
901 GAAATCTGGT CCACGCAGCA TACTTCCTTT TGGTGGGTAT CCCTGGCCTG GGGCCTACCA
961 TACACTTTTG GCTGGCTTTC CCACTGTGTT TTATGTATGC CTTGGCCACC CTGGGTAACC
1021 TGACCATTGT CCTCATCATT CGTGTGGAGA GCGACTGCA TGAGCCCATG TACCTCTTCC
1081 TGGCCATGCT TTCCACTATT GACCTAGTCC TCTCCTCTAT CACCATGCCC AAGATGGCCA
1141 GTCTTTTCTT GATGGGCATC CAGGAGATCG AGTTCAACAT TTGCCTGGCC CAGATGTTCC
1201 TTATCCATGC TCTGTCAGCC GTGGAGTCAG CTGTCCTGCT GGCCATGGCT TTTGACCGCT

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1261 TTGTGGCCAT TTGCCACCCA TTGCGCCATG CTTCTGTGCT GACAGGGTGT ACTGTGGCCA
 1321 AGATTGGACT ATCTGCCCTG ACCAGGGGGT TTGTATTCTT CTTCCCACTG CCCTTCATCC
 1381 TCAAGTGGTT GTCCTACTGC CAAACACATA CTGTCACACA CTCCTTCTGT CTGCACCAAG
 1441 ATATTATGAA GCTGTCCTGT ACTGACACCA GGGTCAATGT GGTTTATGGA CTCTTCATCA
 1501 TCCTCTCAGT CATGGGTGTG GACTCTCTCT TCATTGGCTT CTCATATATC CTCATCCTGT
 1561 GGGCTGTTTT GGAGCTGTCC TCTCGGAGGG CAGCACTCAA GGCTTTCAAC ACCTGCATCT
 1621 CCCACCTCTG TGCTGTTCTG GTCTTCTATG TACCCCTCAT TGGGCTCTCG GTGGTGCATA
 1681 GGCTGGGTGG TCCCACCTCC CTCCTCCATG TGGTTATGGC TAATACCTAC TTGCTGCTAC
 1741 CACCTGTAGT CAACCCCTT GTCTATGGAG CCAAGACCAA AGAGATCTGT TCAAGGGTCC
 1801 TCTGTATGTT CTCACAAGGT GGCAAGTGAG ACACCTTAGT GTCTCGCTTC TACTACTACT
 1861 ACAGAAGATG GGAATATTAG GATCCTATTG AATGCCTTGG TGATTAAAGT ATCAAACCTA
 1921 TTGTGCTGTC TTCTTCCAGC AATTTAAGTA GATCATGTAT TCTGTCTCCA GGAATGTGTC
 1981 AGTACTGAAC TTATGACCCT GTCTGGACAT CCTGGAGAAT GACTGCACTA GTCCCTCTGC
 2041 TATGGTGGTC TTGCCTTCTC CTTCTCTCTC AGCTAGAAAA TACATCTAGT TTTGACATGG
 2101 GGAGGCTGTA AAGATCACAC CTCATGGTTC ATTCCAGTTT TGAAGTATGA TTTTAATGTT
 2161 CTTGCCCCCA TGTGCCCATG TTGGTGAATT TGCATGGACT ATAAACGTTA TTGCAAATAC
 2221 CCTAAAGTGG TTACCCAGCC ATAATCAGGG GTTAATGAAG GTATTTGGGG AATAGTAACT
 2281 GGAGAGACAG CAACAAGACA AGAGGCAGCT CACATGCAAT GTTGAAGTTT CTGTATGCAA
 2341 GAGGGTGTGT TGGCAGATTT GTGAAATCTG CCCATTTGCA TCTGTATGGC TCTATATGAC
 2401 TATTTGTCCA TAAGGGTGCC ATGTATTCTG GTTGTGGGTG TGAATGTGTG GGTGTGTTTA
 2461 TGTGGACACT TGCTTTTCAG TGTGCGTATA TGTGAGAGAG AGGGTGCACA CATGGAATAC
 2521 GTACTGGTTG TGTCTGGTG AGTGTGGTAG CTATGTCCTG GCACATGTAT GTTTCATGAG
 2581 ACGTGTCTCT GATTGCGCAT TTGTATTTCT GTGGTATCTG TTAGTTGGTA TATGATATGT
 2641 GTCTACGTGA GAATGCTGGT GTCTGTATCT GCATGGTGGG CAGTACCTTT ATGTGTATCT
 2701 GGTAAGAATG CTGCCTCTAC CTTTTCTTCC TATTTGTACT ATGTGAATGT GGTGCATGAA
 2761 TGTGTGGAAT GTGTGGAATG TGTAGTATTG GGATGCCTGT ATCTTTCAGC GTGTTTGGGT
 2821 GTATGTCCAC TGTGCATAAT ATTTGAGATG TAAAACCATT TTGTGCGGTA TATGTGTTAT
 2881 TAGTTGTAAG TCGGTGAAAT GTACATCTGA ATTCTGTGTG CATATTGTTG GTACTGATGC
 2941 TATTTTCGTG CATATGTCTA GTGTATATGT TTTAAGGCAA ACTTTCTTTG TGTGTTGGGT
 3001 GTGTATGTGA CACGAATGGG GACAGCATCT GTATTTCTGA GCATGGATTG ATGTGTGGTG
 3061 TCTGTATGTA TCTTGGAATG GAGGAGGGAG ATTGAAGAAG TCTGGCTGTG AGCAGCAGAA
 3121 ATAATTTCCA AAGTTGAGTG ACATGACTCT AAGATGCCCA GTTCTCGGC CTGGGGTCAG
 3181 CCTGGGTGAT AGCTCAGTCT GTCAGAATGA AAGGAAACAC GGTGCTTCCT TGCTCCACCT
 3241 TTTCACAGGC CAGACCACAC CTTCTTCATC CTGAACACAA GGATTTCAAG GGCTTTTGTT
 3301 ACCTCTTCCT ACGTTTCCTG CCTCTGCTAT CCGAGGCACT GGCCTCCCTA AACCTGCCC
 3361 TCCTGCCTCA ATAGCAAGTC ATGGTATCCT CACCTCTCCC TTCCCTTTTT GGCTTATCTG
 3421 **CCAAACATGT ATAAAGTCC TTGGTTCCCC ATCTCTACTA AAAATACAAC** AATTAGCCGG
 3481 GTGTGATGGC GCGTGCCTGT AGTCCCAGCT AGTTGGGAGG CTGAGGCAGG AGAAACGCTT
 3541 GAGCCCGCAA GGTGGAGGTT GCAGTGAGCC GAGATCATGC CACTGCACTC CAGCCTGGTG
 3601 ACAGAGCAAG ACTCTGTGTC AAAAAAAAAA AAAAAAAAAA AGCCTTGGTT GTAGGGAGTT
 3661 TCTCCTAATC CCTCTGGGAA AGCAAGGGTG GAGGGGAAGC CAGTCAATCT CCCTTCTGTT
 3721 GCCGCATGGA AACTCCCTTA AGGCAGGAAG CTGAAAAAAC TGTAGCATTC ACCTCATTAT
 3781 TCACCTTGTC TCATGTCTCA CTGTCCTTCC ACATGTCTCA TTGTTACTCC ATATTGGATG
 3841 GAAGTAGAAG TCCCTTTGGT ATTTTAAAA GTCTTTGCCA TGTCTAAGTT AATGAGGTTA
 3901 ATGGAGGCAG CAGAGATGGC TCCAGGGTTC TGATAGCAAG TGTCAGGCTG CGTGCTCTGT
 3961 AGGCACCAGA AACTGTTGTC ACCAGTAATT TTGATGTGGT CTGAGTTAGA ATGGTCTGAT
 4021 TTGCCATGAT CTATTTAACA TAGCTTGATT TAGCGTGTCC TGTGTTCTGA ATTTAAAACT
 4081 CACAGTTGTG **AAACTGATCA GTAAAAAATA AGGGGAGACC AACTAAAAAC CATGTTGTTC**
 4141 **TATTTATAGA** TGTAATTTTT ACTTATTTCA AAATACGAGG TATTTAGTTT TACATTCAAA
 4201 TTGTTCTCTA ACTCTCTAAA ATGTTCTCTG ACTATTTTGG CCCTTAAGGG AGAAACCAGA
 4261 TGTCATTGGT CTTACGTGGC TGGTGTGTTGGG GGTGGGGAGG GTTAAAGAAA CCACGTTCTC
 4321 TGTCCTCAGC CAGAAGTTCA GTAATCCAAG GCCAGAGAGT GGACGGCAGA GGCCTGTCC
 4381 CTGGGGACCT TGGTTATAAG TTATCCAGAC ACAGGGACCA GAGCCTGGGA GACAAAAAAA
 4441 GATGTAGCCC TAGGGCTTTG GGAAAAGGAG GATGGACCCA GTGAATTCCA CGCTTAGCAA

4501 GGACCTAAAC AGTGTCCCCC AAATGAGAGA AGGGAGGACA GAAAGAACAC TTCAGGATGG
 4561 AAATGGGCTG AACTTAAACC GTGGAGTGTC TCTGCAAACT TCCTTTGCCA TTCTCCTGTT
 4621 TGAGTTTGAT AAACCTGAGA AGAGACTTGG ATAAAGACCG TCACGAAGAC TACACTAATG
 4681 AGTTTCTTCT AGCTTTTTTC TACTACTTTT CCCTATCTAT CCTTCACATT GGGAGTTGGC
 4741 ATGAGGATCC CAGCAGCCCA TCAGGGGAGG ACTCTAGAGA TCCCTTTCCC CATTGCCTCT
 4801 CCTCCCCATA CCCCAGGCA TATCCTCCCA GGGCACGGAA GCTGAGAAGC AGTCCAGAAC
 4861 CACAGTGGGC TAGTGAGGGG TACCTGCTGA TGTACCCTTT GGACAGCATT CTGCCCCACC
 4921 CTGCAGGAAG AAGCAGAAGG AGGGAGAGGG TGAGGCAGAG AATAAATAAC CCTGACCAGG
 4981 GAGGTCCAAG GGAGTAGGCG GAGAcagaga ggctgtattt cagtgcagcc tgccagacct

Note: The three high score predictions of promoters were bold and underlined. The lower case sequence indicates the beginning part of the transcript of 101P3A11 gene.--

Please replace Table XXX, beginning at page 214, line 35, with the following rewritten

Table XXX:

--Table XXX: Promoters and their positions predicted by Neural Network Promoter Prediction computer program. (various portions of SEQ ID NO: 2867, respectively, in order of appearance)

Start	End	Score	Promoter Sequence
25	75	0.91	TTTTGCATTTTTTAATAGAGGCAGGGTTTCACCATGTTGGCCTGGCTGGTC
665	715	0.95	CAGGAAGTTGTATATAAGGAGAATCAGAGCAGAGAGAGACTAGGGTTCAG
2477	2527	0.91	TCAGTGTGCGTATATGTGAGAGAGAGGGTGCACACATGGAATACGTA CTG
3139	3189	0.82	TGACATGACTCTAAGATGCCCAGTTTCTCGGCCTGGGGTCAGCCTGGGTG
3420	3470	0.96	GCCAAACATGTATAAAAGTCCTTGGTTCCCCATCTCTACTAAAAATACAA
4092	4142	0.99	AACTGATCAGTAAAAAATAAGGGGAGACCAACTAAAAACCATGTTGTTCT
4953	5003	0.97	AGGCAGAGAATAAATAACCCTGACCAGGGAGGTCCAAGGGAGTAGGCGGA--

Please replace Table XXXI, beginning at page 215, line 1, with the following rewritten

Table XXXI:

--Table XXXI: Alignment of five homologous 5' upstream genomic regulatory regions of the human 101P3A11 and PSA genes.

Query: 5' upstream regulatory region of the PSA gene

Subject: Putative 5' upstream regulatory region of the 101P3A11 gene.

Nucleic acid sequences predicted to be binding sites for the indicated transcription factors are **bolded**, underlined, or *italicized*.

1. NF-1 SP-1 NF-1

Query: 3864 ccaggctggagtg**cagtg**ggcgcagctctcggtcactgcaacctctgcctcccaggttcaa 3923
 (SEQ ID NO: 2868)

Sbjct: 3598 ccaggctggagtg**cagtg**ggcatgatctcggtcactgcaacctccaccttgcggggtcaa 3539
 (SEQ ID NO: 2869)

Query: 3924 gtagttctcctgcctcagcctcctgagttgctgggattacaggcatgcagcaccatgccc 3983

Sbjct: 3538 gcgtttctcctgcctcagcctcccaactagctgggactacaggcacgcgcatcacaccc 3479

Query: 3984 agctaatttttgtagtttttagtagagatgggg 4015

Sbjct: 3478 ggctaattgttgatatttttagtagagatgggg 3447

2.

Query: 4670 cctgtaatcccagctactgaggaggctgaggcaggagaatcacttgaacccagaaggcag 4729
(SEQ ID NO: 2870)

Sbjct: 3496 cctgtagtcccagctagttgggaggctgaggcaggagaaacgcttgagcccgcaaggtgg 3555
(SEQ ID NO: 2871)

NF-1
NF-1
GR
NF-E
GR

Query: 4730 aggttgcaatgagccgagattg**gccactg**cactccagcctggggtgacagagtgagactc 4789

Sbjct: 3556 aggttgcaagtgagccgagatcat**gccactg**cactccagcct-ggtgacagagcaagactc 3614

```
Query: 4790  tgtctcaaaaaaaaaaaaaa 4807
           ||| |||||
Sbjct: 3615  tgtgtcaaaaaaaaaaaaaa 3632
```

3.

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          GR              NF-1 SP1
Query: 142   tgagactgagtcctgctctgtgcccaggctggagtgcagttgcaaccttggtcactg 201
(SEQ ID NO: 2872)

      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 3621 tgacacagagtcttgctctgtccaccaggctggagtgcagttgcatgatctcggtcactg 3562
(SEQ ID NO: 2873)

```

Query: 202 caagctcgcctcctgggttcacgccattctcctgcctcagcctcctgagttagctgggac 261
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 3561 caacctccacttgcggttcaagcgtttctcctgcctcagcctcccaactagctgggac 3502

NF-1

```
Query: 262  tacaggcacccgcccaccacgcctggcctaannnnnnngtatttttagtagagatgggg 318
          |||||
Sbjct: 3501  tacaggcacgcgccatcacaccggcgtaa--ttgttgatttttagtagagatgggg 3447
```

4.

Query: 300 attttagtagagatggggtttcactgtgtagccaggatgggtctcagtctcctgacctc 359
(SEQ ID NO: 2874)

Sbjct: 31 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 atttttaatagaggcagggtttccaccatggtggcctggctggtctgaacccctgacctt 90
 (SEQ ID NO: 2875)

		SP1		NF-1
		LF-A1	CP2	
Query:	360	gtgatctgcccaccttggcctcccaaagtgctgggattacaggcgtgagccactgtgcgcct		419
Sbjct:	91	gcgatctgcccacctcggcctcccaaagtgctgggattacaggcgtgagccactgtacct		150

```

      NF-1
Query: 420 ggc 422
      |||
Sbjct: 151 ggc 153

```

5.

NF-1
CP2

Query: 4506 gccaggcacagtggtcacgcctgtaatcccaacaccatgggaggctgagatgggtggat 4565
(SEQ ID NO: 2876)

||||| ||||||| ||||||| ||||||| ||| ||||||| ||| |||
Sbjct: 153 gccaggtaacagtggtcacgcctgtaatccagcactttgggaggccgaggtgggcagat 94
(SEQ ID NO: 2877)

Query: 4566 cacgaggtcaggagtttgagaccagcctgaccaacatggtgaaactctgtctcta 4620

| | ||||||| ||| ||||||| | ||||||| ||| |||
Sbjct: 93 cgcaaggtcaggggttcgagaccagccaggccaacatggtgaaaccctgcctcta 39--